FIG. 35

EcoRI

```
  1  AATTCGAGCA GAAGCTGATC TCTGAGGAGG ATCTGTAGGG TGGTGGCTCT
     TTAAGCTCGT CTTCGACTAG AGACTCCTCC TAGACATCCC ACCACCGAGA

 51  GGTTCCGGTG ATTTTGATTA TGAAAAGATG GCAAACGCTA ATAAGGGGGC
     CCAAGGCCAC TAAAACTAAT ACTTTTCTAC CGTTTGCGAT TATTCCCCCG

101  TATGACCGAA AATGCCGATG AAAACGCGCT ACAGTCTGAC GCTAAAGGCA
     ATACTGGCTT TTACGGCTAC TTTTGCGCGA TGTCAGACTG CGATTTCCGT

151  AACTTGATTC TGTCGCTACT GATTACGGTG CTGCTATCGA TGGTTTCATT
     TTGAACTAAG ACAGCGATGA CTAATGCCAC GACGATAGCT ACCAAAGTAA

201  GGTGACGTTT CCGGCCTTGC TAATGGTAAT GGTGCTACTG GTGATTTTGC
     CCACTGCAAA GGCCGGAACG ATTACCATTA CCACGATGAC CACTAAAACG

251  TGGCTCTAAT TCCCAAATGG CTCAAGTCGG TGACGGTGAT AATTCACCTT
     ACCGAGATTA AGGGTTTACC GAGTTCAGCC ACTGCCACTA TTAAGTGGAA

              XmnI

301  TAATGAATAA TTTCCGTCAA TATTTACCTT CCCTCCCTCA ATCGGTTGAA
     ATTACTTATT AAAGGCAGTT ATAAATGGAA GGGAGGGAGT TAGCCAACTT
```

FIG. 35A-1

```
351   TGTCGCCCTT   TTGTCTTTGG   CGCTGGTAAA   CCATATGAAT   TTTCTATTGA
      ACAGCGGGAA   AACAGAAACC   GCGACCATTT   GGTATACTTA   AAAGATAACT

401   TTGTGACAAA   ATAAACTTAT   TCCGTGGTGT   CTTTGCGTTT   CTTTTATATG
      AACACTGTTT   TATTTGAATA   AGGCACCACA   GAAACGCAAA   GAAAATATAC

451   TTGCCACCTT   TATGTATGTA   TTTTCTACGT   TTGCTAACAT   ACTGCGTAAT
      AACGGTGGAA   ATACATACAT   AAAAGATGCA   AACGATTGTA   TGACGCATTA

                   HindIII
                   ~~~~~
501   AAGGAGTCTT   GATAAGCTTG   ACCTGTGAAG   TGAAAAATGG   CGCAGATTGT
      TTCCTCAGAA   CTATTCGAAC   TGGACACTTC   ACTTTTTACC   GCGTCTAACA

                                            PacI                FseI
                                            ~~~~~~~~            ~~~~~~~~
551   GCGACATTTT   TTTGTCTGC    CGTTTAATTA   AAGGGGGGGG   GGGGCCGGCC
      CGCTGTAAAA   AAAACAGACG   GCAAATTAAT   TTCCCCCCCC   CCCCGGCCGG

             BsrGI
             ~~~~~
601   TGGGGGGGGG   TGTACATGAA   ATTGTAAACG   TTAATATTTT   GTTAAAATTC
      ACCCCCCCCC   ACATGTACTT   TAACATTTGC   AATTATAAAA   CAATTTTAAG
```

FIG. 35A-2

```
651  GCGTTAAATT TTTGTTAAAT CAGCTCATTT TTTAACCAAT AGGCCGAAAT
     CGCAATTTAA AAACAATTTA GTCGAGTAAA AAATTGGTTA TCCGGCTTTA

701  CGCAAAATC  CCTTATAAAT CAAAAGAATA GACCGAGATA GGGTTGAGTG
     GCCGTTTTAG GGAATATTTA GTTTTCTTAT CTGGCTCTAT CCCAACTCAC

751  TTGTTCCAGT TTGGAACAAG AGTCCACTAT TAAAGAACGT GGACTCCAAC
     AACAAGGTCA AACCTTGTTC TCAGGTGATA ATTTCTTGCA CCTGAGGTTG

801  GTCAAAGGGC GAAAAACCGT CTATCAGGGC GATGGCCCAC TACGAGAACC
     CAGTTTCCCG CTTTTTGGCA GATAGTCCCG CTACCGGGTG ATGCTCTTGG

851  ATCACCCTAA TCAAGTTTTT TGGGGTCGAG GTGCCGTAAA GCACTAAATC
     TAGTGGGATT AGTTCAAAAA ACCCCAGCTC CACGGCATTT CGTGATTTAG
                                     BanII
                                     ~~~~~

901  GGAACCCTAA AGGGAGCCCC CGATTTAGAG CTTGACGGGG AAAGCCCGCG
     CCTTGGGATT TCCCTCGGGG GCTAAATCTC GAACTGCCCC TTTCGGCCGC

951  AACGTGGCGA GAAAGGAAGG GAAGAAAGCG AAAGGAGCGG GCGCTAGGGC
     TTGCACCGCT CTTTCCTTCC CTTCTTTCGC TTTCCTTCGC CGCGATCCCG
```

FIG. 35A-3

```
1001   GCTGGCAAGT  GTAGCGGTCA  CGCTGCGCGT  AACCACCACA  CCCGCGCGC
       CGACCGTTCA  CATCGCCAGT  GCGACGCGCA  TTGGTGGTGT  GGGCGGGCG

                                            NheI
                                            ~ ~ ~ ~

1051   TTAATGCGCC  GCTACAGGGC  GCGTGCTAGC  CATGTGAGCA  AAAGGCCAGC
       AATTACGCGG  CGATGTCCCG  CGCACGATCG  GTACACTCGT  TTTCCGGTCG

1101   AAAAGGCCAG  GAACCGTAAA  AAGGCCCGT   TGCTGGCGTT  TTTCCATAGG
       TTTTCCGGTC  CTTGGCATTT  TTCCGGGCGCA ACGACCGCAA  AAAGGTATCC

1151   CTCCGCCCCC  CTGACGAGCA  TCACAAAAAT  CGACGCTCAA  GTCAGAGGTG
       GAGGCGGGGG  GACTGC??GT  AGTGTTTTTA  GCTGCGAGTT  CAGTCTCCAC

1201   GCGAAACCCG  ACAGGACTAT  AAAGATACCA  GGCGTTTCCC  CCTGGAAGCT
       CGCTTTGGGC  TGTCCTGATA  TTTCTATGGT  CCGCAAAGGG  GGACCTTCGA

       BsssI
       ~ ~ ~ ~

1251   CCCTCGTGCG  CTCTCCTGTT  CCGACCCTGC  CGCTTACCGG  ATACCTGTCC
       GGGAGCACGC  GAGAGGACAA  GGCTGGGACG  GCGAATGGCC  TATGGACAGG

1301   GCCTTTCTCC  CTTCGGGAAG  CGTGGCGCTT  TCTCATAGCT  CACGCTGTAG
       CGGAAAGAGG  GAAGCCCTTC  GCACCGCGAA  AGAGTATCGA  GTGCGACATC
```

FIG. 35A-4

```
1351  GTATCTCAGT TCGGTGTAGG TCGTTCGCTC CAAGCTGGGC TGTGTGCACG
      CATAGAGTCA AGCCACATCC AGCAAGCGAG GTTCGACCCG ACACACGTGC

1401  AACCCCCCGT TCAGCCCGAC CGCTGCGCCT TATCCGGTAA CTATCGTCTT
      TTGGGGGGCA AGTCGGGCTG GCGACGCGGA ATAGGCCATT GATAGCAGAA

1451  GAGTCCAACC CGGTAAGACA CGACTTATCG CCACTGGCAG CAGCCACTGG
      CTCAGGTTGG GCCATTCTGT GCTGAATAGC GGTGACCGTC GTCGGTGACC

1501  TAACAGGATT AGCAGAGCGA GGTATGTAGG CGGTGCTACA GAGTTCTTGA
      ATTGTCCTAA TCGTCTCGCT CCATACATCC GCCACGATGT CTCAAGAACT

1551  AGTGGGTGGCC TAACTACGGC TACACTAGAA GAACAGTATT TGGTATCTGC
      TCACCACCGG ATTGATGCCG ATGTGATCTT CTTGTCATAA ACCATAGACG

1601  GCTCTGCTGT AGCCAGTTAC CTTCGGAAAA AGAGTTGGTA GCTCTTGATC
      CGAGACGACA TCGGTCAATG GAAGCCTTTT TCTCAACCAT CGAGAACTAG

1651  CGGCAAACAA ACCACCGCTG GTAGCGGTGG TTTTTTTGTT TGCAAGCAGC
      GCCGTTTGTT TGGTGGCGAC CATCGCCACC AAAAAAACAA ACGTTCGTCG

1701  AGATTACGCG CAGAAAAAAA GGATCTCAAG AAGATCCTTT GATCTTTTCT
      TCTAATGCGC GTCTTTTTTT CCTAGAGTTC TTCTAGGAAA CTAGAAAGA
```

FIG. 35A-5

```
1751   ACGGGGTCTG   ACGCTCAGTG   GAACGAAAAC   TCACGTTAAG   GGATTTTGGT
       TGCCCCAGAC   TGCGAGTCAC   CTTGCTTTTG   AGTGCAATTC   CCTAAAACCA

              BglII
              ~~~~~~

1801   CAGATCTAGC   ACCAGGCGTT   TAAGGGCACC   AATAACTGCC   TTAAAAAAAT
       GTCTAGATCG   TGGTCCGCAA   ATTCCCGTGG   TTATTGACGG   AATTTTTTTA

1851   TACGCCCCGC   CCTGCCACTC   ATCGCAGTAC   TGTTGTAATT   CATTAAGCAT
       ATGCGGGGCG   GGACGGTGAG   TAGCGTCATG   ACAACATTAA   GTAATTCGTA

1901   TCTGCCGACA   TGGAAGCCAT   CACAAACGGC   ATGATGAACC   TGAATCGCCA
       AGACGGCTGT   ACCTTCGGTA   GTGTTTGCCG   TACTACTTGG   ACTTAGCGGT

1951   GCGGCATCAG   CACCTTGTCG   CCTTGCGTAT   AATATTTGCC   CATAGTGAAA
       CGCCGTAGTC   GTGGAACAGC   GGAACGCATA   TTATAAACGG   GTATCACTTT

2001   ACGGGGGCGA   AGAAGTTGTC   CATATTGGCT   ACGTTTAAAT   CAAAACTGGT
       TGCCCCCGCT   TCTTCAACAG   GTATAACCGA   TGCAAATTTA   GTTTTGACCA

2051   GAAACTCACC   CAGGGATTGG   CTGAGACGAA   AAACATATTC   TCAATAAACC
       CTTTGAGTGG   GTCCCTAACC   GACTCTGCTT   TTTGTATAAG   AGTTATTTGG
```

FIG. 35A-6

```
2101  CTTTAGGGAA  ATAGGCCAGG  TTTTCACCGT  AACACGCCAC  ATCTTGCGAA
      GAAATCCCTT  TATCCGGTCC  AAAAGTGGCA  TTGTGCGGTG  TAGAACGCTT

2151  TATATGTGTA  GAAACTGCCG  GAAATCGTCG  TGGTATTCAC  TCCAGAGCGA
      ATATACACAT  CTTTGACGGC  CTTTAGCAGC  ACCATAAGTG  AGGTCTCGCT

2201  TGAAAACGTT  TCAGTTTGCT  CATGGAAAAC  GGTGTAACAA  GGGTGAACAC
      ACTTTTGCAA  AGTCAAACGA  GTACCTTTTG  CCACATTGTT  CCCACTTGTG

2251  TATCCCATAT  CACCAGCTCA  CCGTCTTTCA  TTGCCATACG  GAACTCCGGG
      ATAGGGTATA  GTGGTCGAGT  GGCAGAAAGT  AACGGTATGC  CTTGAGGCCC

2301  TGAGCATTCA  TCAGGCGGGC  AAGAATGTGA  ATAAAGGCCG  GATAAAACTT
      ACTCGTAAGT  AGTCCGCCCG  TTCTTACACT  TATTTCCGGC  CTATTTTGAA

2351  GTGCTTATTT  TTCTTTACGG  TCTTTAAAAA  GGCCGTAATA  TCCAGCTGAA
      CACGAATAAA  AAGAAATGCC  AGAAATTTTT  CCGGCATTAT  AGGTCGACTT

2401  CGGTCTGGTT  ATAGGTACAT  TGAGCAACTG  ACTGAAATGC  CTCAAAATGT
      GCCAGACCAA  TATCCATGTA  ACTCGTTGAC  TGACTTTACG  GAGTTTTACA

2451  TCTTTACGAT  GCCATTGGGA  TATATCAACG  GTGGTATATC  CAGTGATTTT
      AGAAATGCTA  CGGTAACCCT  ATATAGTTGC  CACCATATAG  GTCACTAAAA
```

FIG. 35A-7

```
2501  TTTCTCCATT TTAGCTTCCT TAGCTCCTGA AAATCTCGAT AACTCAAAAA
      AAAGAGGTAA AATCGAAGGA ATCGAGGACT TTTAGAGCTA TTGAGTTTTT

2551  ATACGCCCGG TAGTGATCTT ATTTCATTAT GGTGAAAGTT GGAACCTCAC
      TATGCGGGCC ATCACTAGAA TAAAGTAATA CCACTTTCAA CCTTGGAGTG
                    AatII

2601  CCGACGTCTA ATGTGAGTTA GCTCACTCAT TAGGCACCCC AGGCTTTACA
      GGCTGCAGAT TACACTCAAT CGAGTGAGTA ATCCGTGGGG TCCGAAATGT

2651  CTTTATGCTT CCGGCTCGTA TGTTGTGTGG AATTGTGAGC GGATAACAAT
      GAAATACGAA GGCCGAGCAT ACAACACACC TTAACACTCG CCTATTGTTA
                                        XbaI    SphI

2701  TTCACACAGG AAACAGCTAT GACCATGATT ACGAATTTCT AGAGCATGCG
      AAGTGTGTCC TTTGTCGATA CTGGTACTAA TGCTTAAAGA TCTCGTACGC
          EcoRI

2751  GGGGG
      CCCCC
```

FIG. 35A-8

AatII (6)

XbaI (128)

XmnI (136)

LACZ'

SphI (173)
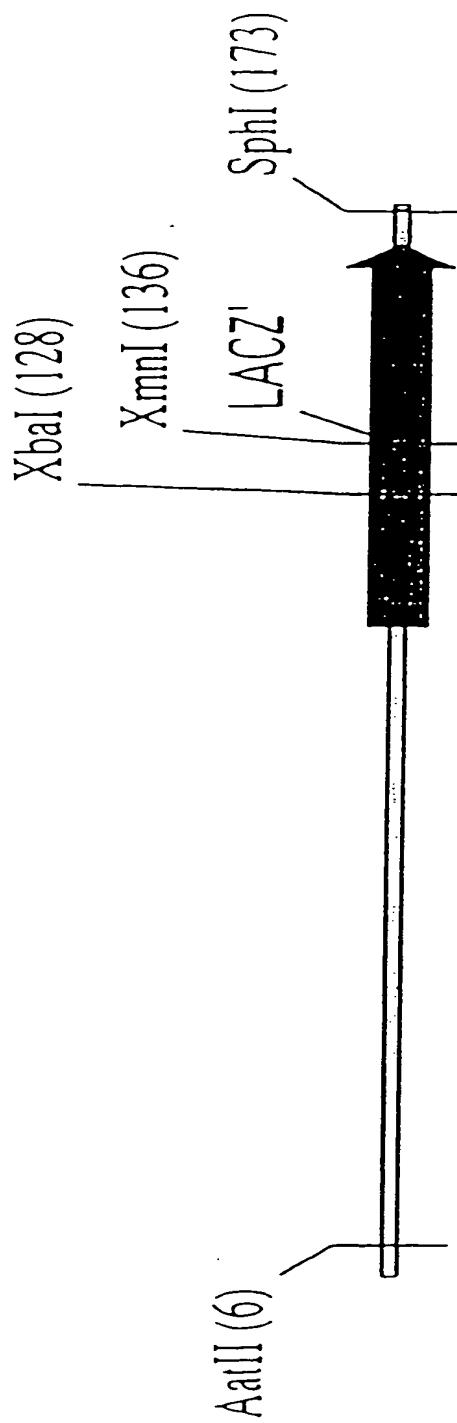
M2
173 bp

FIG. 35A-9

M 2:

```
      AatII
      ------
  1   GACGTCTTAA TGTGAGTTAG CTCACTCATT AGGCACCCCA GGCTTTACAC
      CTGCAGAATT ACACTCAATC GAGTGAGTAA TCCGTGGGGT CCGAAATGTG

 51   TTTATGCTTC CGGCTCGTAT GTTGTGTGGA ATTGTGAGCG GATAACAATT
      AAATACGAAG GCCGAGCATA CAACACACCT TAACACTCGC CTATTGTTAA

                                                  XmnI
                                                  ----
                                      XbaI
                                      ----
101   TCACACAGGA AACAGCTATG ACCATGTCTA GAATAACTTC GTATAATGTA
      AGTGTGTCCT TTGTCGATAC TGGTACAGAT CTTATTGAAG CATATTACAT

                           SphI
                           ----
151   CGCTATACGA AGTTATCGCA TGC
      GCGATATGCT TCAATAGCGT ACG
```

FIG. 35A-10

M3
47 bp

FIG. 35A-11

AatII (47)
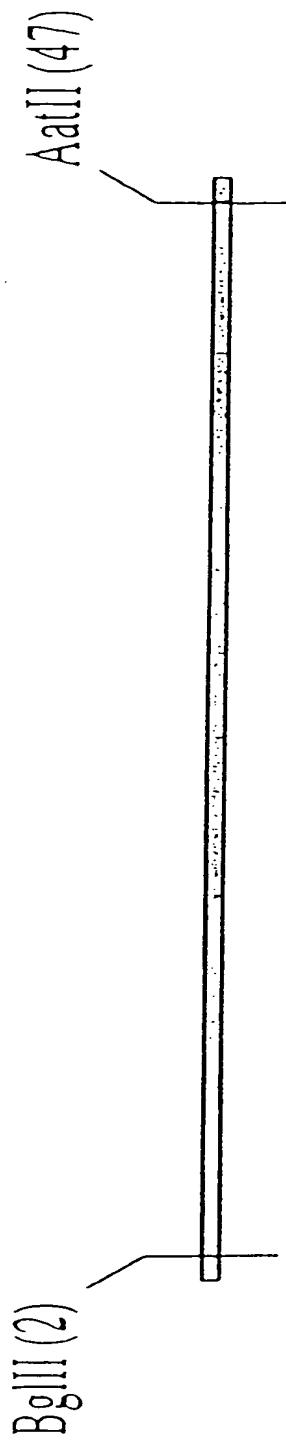
BglII (2)

M 3 :

```
        BglII                                              AatII
        ' ' ' ' '                                          ' ' ' '
1   AGATCTCATA  ACTTCGTATA  ATGTATGCTA  TACGAAGTTA  TGACGTC
    TCTAGAGTAT  TGAAGCATAT  TACATACGAT  ATGCTTCAAT  ACTGCAG
```

FIG. 35A-12

GGGGS-linker
EcoRI (2)

gIII long

XmnI (1046)

HindIII (1251)
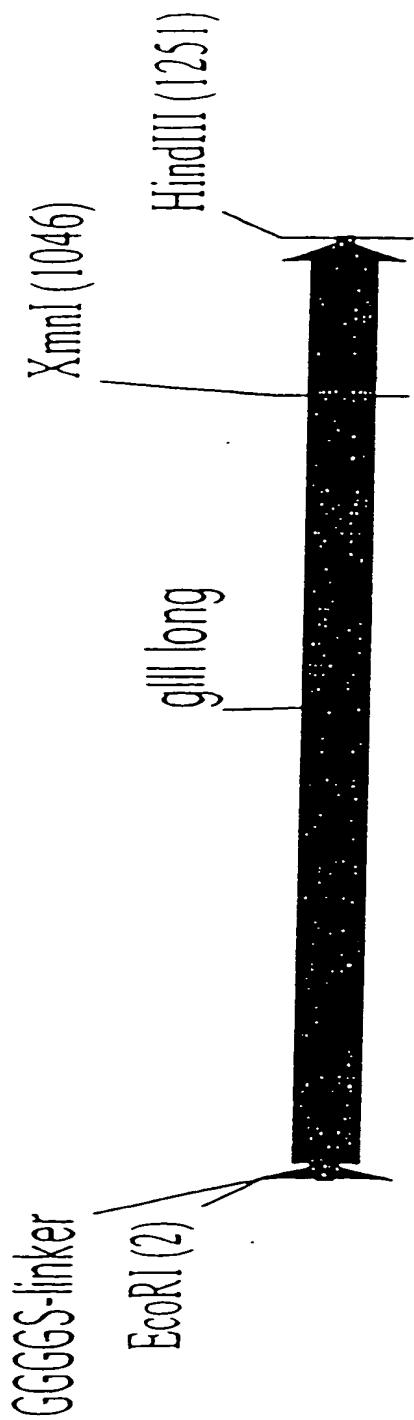
M7-1 (long)
1255 bp
FIG. 35A-13

M 7-I (long):

```
    EcoRI
    - - - - -
1   GAATTCGGTG  GTGGTGGATC  TGCGTGCGCT  GAAACGGGTTG  AAAGTTGTTT
    CTTAAGCCAC  CACCACCTAG  ACGCACGCGA  CTTTGCCAAC   TTTCAACAAA

51  AGCAAAAATCC CATACAGAAA  ATTCATTTAC  TAACGTCTGG   AAAGACGACA
    TCGTTTTTAGG GTATGTCTTT  TAAGTAAATG  ATTGCAGACC   TTTCTGCTGT

101 AAACTTTAGA  TCGTTACGCT  AACTATGAGG  GCTGTCTGTG   GAATGCTACA
    TTTGAAATCT  AGCAATGCGA  TTGATACTCC  CGACAGACAC   CTTACGATGT

151 GGCGTTGTAG  TTTGTACTGG  TGACGAAACT  CAGTGTTACG   GTACATGGGT
    CCGCAACATC  AAACATGACC  ACTGCTTTGA  GTCACAATGC   CATGTACCCA

201 TCCTATTGGG  CTTGCTATCC  CTGAAAATGA  GGGTGGTGGC   TCTGAGGGTG
    AGGATAACCC  GAACGATAGG  GACTTTTACT  CCCACCACCG   AGACTCCCAC

251 GCGGTTCTGA  GGGTGGCGGT  TCTGAGGGTG  GCGGTACTAA   ACCTCCTGAG
    CGCCAAGACT  CCCACCGCCA  AGACTCCCAC  CGCCATGATT   TGGAGGACTC

301 TACGGTGATA  CACCTATTCC  GGGCTATACT  TATATCAACC   CTCTCGACGG
    ATGCCACTAT  GTGGATAAGG  CCCGATATGA  ATATAGTTGG   GAGAGCTGCC
```

FIG. 35A-14

```
351  CACTTATCCG CCTGGTACTG AGCAAAACCC CGCTAATCCT AATCCTTCTC
     GTGAATAGGC GGACCATGAC TCGTTTTGGG GCGATTAGGA TTAGGAAGAG

401  TTGAGGAGTC TCAGCCTCTT AATACTTTCA TGTTTCAGAA TAATAGGTTC
     AACTCCTCAG AGTCGGAGAA TTATGAAAGT ACAAAGTCTT ATTATCCAAG

451  CGAAATAGGC AGGGGGCATT AACTGTTTAT ACGGGCACTG TTACTCAAGG
     GCTTTATCCG TCCCCCGTAA TTGACAAATA TGCCCGTGAC AATGAGTTCC

501  CACTGACCCC GTTAAAACTT ATTACCAGTA CACTCCTGTA TCATCAAAAG
     GTGACTGGGG CAATTTTGAA TAATGGTCAT GTGAGGACAT AGTAGTTTTC

551  CCATGTATGA CGCTTACTGG AACGGTAAAT TCAGAGACTG CGCTTTCCAT
     GGTACATACT GCGAATGACC TTGCCATTTA AGTCTCTGAC GCGAAAGGTA

601  TCTGGCTTTA ATGAGGATTT ATTTGTTTGT GAATATCAAG GCCAATCGTC
     AGACCGAAAT TACTCCTAAA TAAACAAACA CTTATAGTTC CGGTTAGCAG

651  TGACCTGCCT CAACCTCCTG TCAATGCTGG CGGCGGCTCT GGTGGTGGTT
     ACTGGACGGA GTTGGAGGAC AGTTACGACC GCCGCCGAGA CCACCACCAA

701  CTGGTGGCGG CTCTGAGGGT GGTGGCTCTG AGGGTGGCGG TTCTGAGGGT
     GACCACCGCC GAGACTCCCA CCACCGAGAC TCCCACCGCC AAGACTCCCA
```

FIG. 35A-15

```
 751  GGCGGCTCTG AGGGAGGCGG TTCCGGTGGT GGCTCTGGTT CCGGTGATTT
      CCGCCGAGAC TCCCTCCGCC AAGGCCACCA CCGAGACCAA GGCCACTAAA

 801  TGATTATGAA AAGATGGCAA ACGCTAATAA GGGGGCTATG ACCGAAAATG
      ACTAATACTT TTCTACCGTT TGCGATTATT CCCCCGATAC TGGCTTTTAC

 851  CCGATGAAAA CGCGCTACAG TCTGACGCTA AAGGCAAACT TGATTCTGTC
      GGCTACTTTT GCGCGATGTC AGACTGCGAT TTCCGTTTGA ACTAAGACAG

 901  GCTACTGATT ACGGGTGCTGC TATCGATGGT TTCATTGGTG ACGTTTCCGG
      CGATGACTAA TGCCACGACG ATAGCTACCA AAGTAACCAC TGCAAAGGCC

 951  CCTTGCTAAT GGTAATGGTG CTACTGGTGA TTTTGCTGGC TCTAATTCCC
      GGAACGATTA CCATTACCAC GATGACCACT AAAACGACCG AGATTAAGGG

                                                   XmnI
                                                   |  |  |
1001  AAATGGCTCA AGTCGGTGAA GGTGATAATT CACCTTTAAT GAATAATTTC
      TTTACCGAGT TCAGCCACTT CCACTATTAA GTGGAAATTA CTTATTAAAG

1051  CGTCAATATT TACCTTCCAT CCCTCAATCG GTTGAATGTC GCCCTTTTGT
      GCAGTTATAA ATGGAAGGTA GGGAGTTAGC CAACTTACAG CGGGAAAACA
```

FIG. 35A-16

```
1101   CTTTGGCGCT GGTAAACCCT ATGAATTTTC TATTGATTGT GACAAAATAA
       GAAACCGCGA CCATTTGGGA TACTTAAAAG ATAACTAACA CTGTTTTATT

1151   ACTTATTCCG TGGTGTCTTT GCGTTTCTTT TATATGTTGC CACCTTTATG
       TGAATAAGGC ACCACAGAAA CGCAAAGAAA ATATACAACG GTGGAAATAC

                                                        HindIII
                                                        -------

1201   TATGTATTTT CTACGTTTGC TAACATACTG CGTAATAAGG AGTCTTGATA
       ATACATAAAA GATGCAAACG ATTGTATGAC GCATTATTCC TCAGAACTAT

       HindI
       - - - -

1251   AGCTT
       TCGAA
```

FIG. 35A-17

EcoRI (5)

gIII supershort

XmnI (293)

HindIII (498)
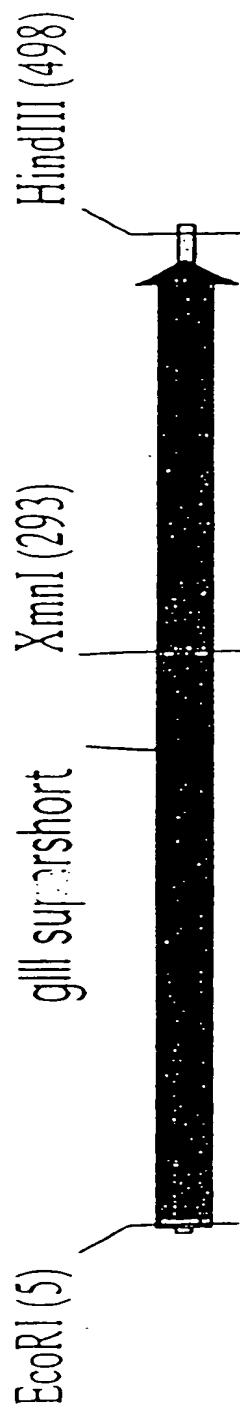
M7-II (ss-TAG)
502 bp

FIG. 35A-18

M 7-II (ss-TAG):

EcoRI
‒ ‒ ‒ ‒ ‒ ‒

1   CGGGAATTCG GAGGCGGTTC CGGTGGTGGC TCTGGTTCCG GTGATTTTGA
     GCCCTTAAGC CTCCGCCAAG GCCACCACCG AGACCAAGGC CACTAAAACT

51   TTATGAAAAG ATGGCAAACG CTAATAAGGG GGCTATGACC GAAAATGCCG
     AATACTTTTC TACCGTTTGC GATTATTCCC CCGATACTGG CTTTTACGGC

101 ATGAAAACGC GCTACAGTCT GACGGCTAAAG GCAAACTTGA TTCTGTCGCT
     TACTTTTGCG CGATGTCAGA CTGCCGATTTC CGTTTGAACT AAGACAGCGA

151 ACTGATTACG GTGCTGCTAT CGATGGTTTC ATTGGTGACG TTTCCGGCCT
     TGACTAATGC CACGACGATA GCTACCAAAG TAACCACTGC AAAGGCCGGA

201 TGCTAATGGT AATGGGTGCTA CTGGTGATTT TGCTGGCTCT AATTCCCAAA
     ACGATTACCA TTACCACGAT GACCACTAAA ACGACCGAGA TTAAGGGTTT

                                        XmnI
                                        ‒ ‒ ‒ ‒
                                        ‒ ‒ ‒ ‒ ‒ ‒ ‒ ‒
251 TGGCTCAAGT CGGTGACGGT GATAATTCAC CTTTAATGAA TAATTTCCGT
     ACCGAGTTCA GCCACTGCCA CTATTAAGTG GAAATTACTT ATTAAAGGCA

FIG. 35A-19

```
301  CAATATTTAC CTTCCCTCCC TCAATCGGTT GAATGTCGCC CTTTTGTCTT
     GTTATAAATG GAAGGGAGGG AGTTAGCCAA CTTACAGCGG GAAAACAGAA

351  TGGCGCTGGT AAACCATATG AATTTTCTAT TGATTGTGAC AAAATAAACT
     ACCGCGACCA TTTGGTATAC TTAAAAGATA ACTAACACTG TTTTATTTGA

401  TATTCCGTGG TGTCTTTGCG TTTCTTTTAT ATGTTGCCAC CTTTATGTAT
     ATAAGGCACC ACAGAAACGC AAAGAAAATA TACAACGGTG GAAATACATA

                                           HindIII
                                           - - - -

451  GTATTTCTA CGTTTGCTAA CATACTGCGT AATAAGGAGT CTTGATAAGC
     CATAAAAGAT GCAAACGATT GTATGACGCA TTATTCCTCA GAACTATTCG

501  Hi         TT
     ~          AA
```

FIG. 35A-20

M8
47 bp

FIG. 35A-21

M 8:
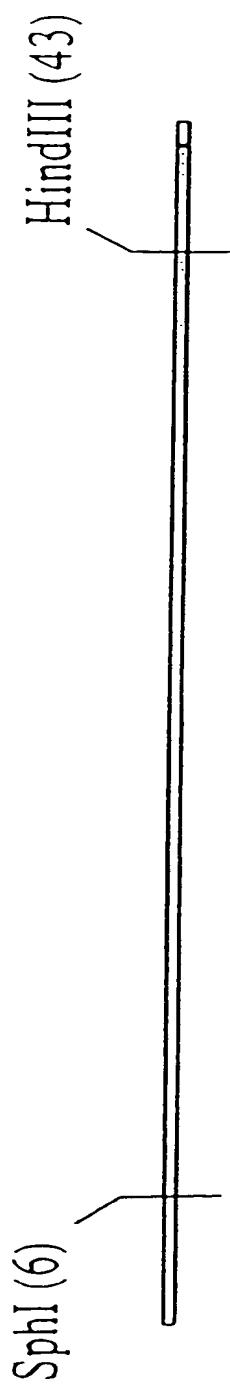
```
         SphI                                              HindIII
         -----                                             -------
1  GCATGCCATA ACTTCGTATA ATGTACGCTA TACGAAGTTA TAAGCTT
   CGTACGGTAT TGAAGCATAT TACATGCGAT ATGCTTCAAT ATTCGAA
```

FIG. 35A-22

M10-II
1163 bp

FIG. 35A-23

BsrGI (7)

XmnI (270)

bla

bla-term

FseI (1140)

PacI (1154)
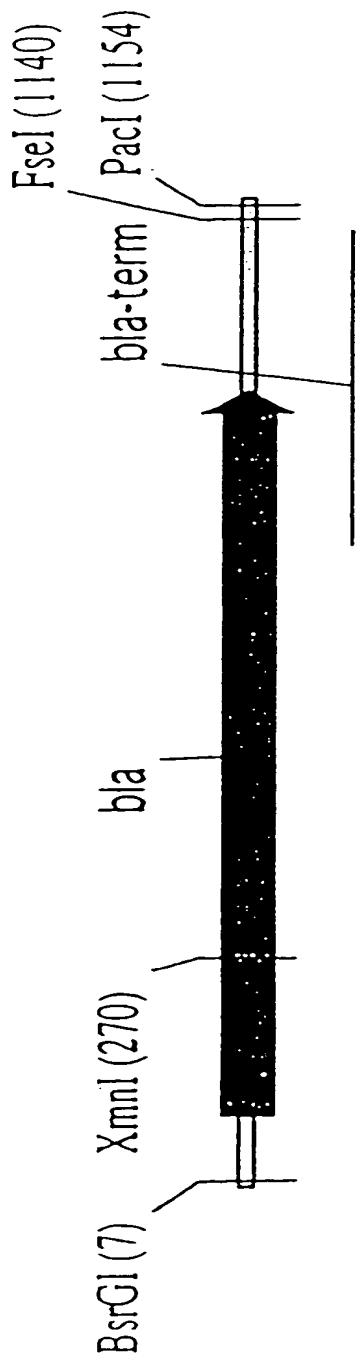
M 10-II:

BsrGI
----

1   GGGGGTGTAC ATTCAAATAT GTATCCGCTC ATGAGACAAT AACCCTGATA
     CCCCCACATG TAAGTTTATA CATAGGCGAG TACTCTGTTA TTGGGACTAT

51   AATGCTTCAA TAATATTGAA AAAGGAAGAG TATGAGTATT CAACATTTCC
     TTACGAAGTT ATTATAACTT TTTCCTTCTC ATACTCATAA GTTGTAAAGG

101 GTGTCGCCCT TATTCCCTTT TTTGCGGCAT TTTGCCTTCC TGTTTTTGCT
     CACAGCGGGA ATAAGGGAAA AAACGCCGTA AAACGGAAGG ACAAAAACGA

151 CACCCAGAAA CGCTGGTGAA AGTAAAAGAT GCTGAGGATC AGTTGGGTGC
     GTGGGTCTTT GCGACCACTT TCATTTTCTA CGACTCCTAG TCAACCCACG

201 GCGAGTGGGT TACATCGAAC TGGATCTCAA CAGCGGTAAG ATCCTTGAGA
     CGCTCACCCA ATGTAGCTTG ACCTAGAGTT GTCGCCATTC TAGGAACTCT

                         XmnI
                         ----

251 GTTTTCGCCC CGAAGAACGT TTTCCAATGA TGAGCACTTT TAAAGTTCTG
     CAAAAGCGGG GCTTCTTGCA AAAGGTTACT ACTCGTGAAA ATTTCAAGAC

FIG. 35A-24

301 CTATGTGGCG CGGTATTATC CCGTATTGAC GCCGGGCAAG AGCAACTCGG
     GATACACCGC GCCATAATAG GGCATAACTG CGGCCCGTTC TCGTTGAGCC

351 TCGCCGCATA CACTATTCTC AGAATGACTT GGTTGAGTAC TCACCAGTCA
     AGCGGCGTAT GTGATAAGAG TCTTACTGAA CCAACTCATG AGTGGTCAGT

401 CAGAAAAGCA TCTTACGGAT GGCATGACAG TAAGAGAATT ATGCAGTGCT
     GTCTTTTCGT AGAATGCCTA CCGTACTGTC ATTCTCTTAA TACGTCACGA

451 GCCATAACCA TGAGTGATAA CACTGCGGCC AACTTACTTC TGACAACGAT
     CGGTATTGGT ACTCACTATT GTGACGCCGG TTGAATGAAG ACTGTTGCTA

501 CGGAGGACCG AAGGAGCTAA CCGCTTTTTT GCACAACATG GGGGATCATG
     GCCTCCTGGC TTCCTCGATT GGCGAAAAAA CGTGTTGTAC CCCCTAGTAC

551 TAACTCGCCT TGATCGTTGG GAACCGGAGC TGAATGAAGC CATACCAAAC
     ATTGAGCGGA ACTAGCAACC CTTGGCCTCG ACTTACTTCG GTATGGTTTG

601 GACGAGCGTG ACACCACGAT GCCTGTAGCA ATGGCAACAA CGTTGCGCAA
     CTGCTCGCAC TGTGGTGCTA CGGACATCGT TACCGTTGTT GCAACGCGTT

651 ACTATTAACT GGCGAACTAC TTACTCTAGC TTCCCGGCAA CAGTTAATAG
     TGATAATTGA CCGCTTGATG AATGAGATCG AAGGGCCGTT GTCAATTATC

FIG. 35A-25

```
701   ACTGGATGGA GGCGGATAAA GTTGCAGGAC CACTTCTGCG CTCGGCCCTT
      TGACCTACCT CCGCCTATTT CAACGTCCTG GTGAAGACGC GAGCCGGGAA

751   CCGGCTGGCT GGTTTATTGC TGATAAATCT GGAGCCGGTG AGCGTGGGTC
      GGCCGACCGA CCAAATAACG ACTATTTAGA CCTCGGCCAC TCGCACCCAG

801   TCGCGGTATC ATTGCAGCAC TGGGGCCAGA TGGTAAGCCC TCCCGTATCG
      AGCGCCATAG TAACGTCGTG ACCCCGGTCT ACCATTCGGG AGGGCATAGC

851   TAGTTATCTA CACGACGGGG AGTCAGGCAA CTATGGATGA ACGAAATAGA
      ATCAATAGAT GTGCTGCCCC TCAGTCCGTT GATACCTACT TGCTTTATCT

901   CAGATCGCTG AGATAGGTGC CTCACTGATT AAGCATTGGG TAACTGTCAG
      GTCTAGCGAC TCTATCCACG GAGTGACTAA TTCGTAACCC ATTGACAGTC

951   ACCAAGTTTA CTCATATATA CTTTAGATTG ATTTAAAACT TCATTTTTAA
      TGGTTCAAAT GAGTATATAT GAAATCTAAC TAAATTTTGA AGTAAAAATT

1001  TTTAAAAGGA TCTAGGTGAA GATCCTTTTT GATAATCTCA TGACCAAAAT
      AAATTTTCCT AGATCCACTT CTAGGAAAAA CTATTAGAGT ACTGGTTTTA

1051  CCCTTAACGT GAGTTTTCGT TCCACTGAGC GTCAGACCCC GTAGAAAAGA
      GGGAATTGCA CTCAAAAGCA AGGTGACTCG CAGTCTGGGG CATCTTTTCT
```

FIG. 35A-26

```
                              FseI              PacI
                            ------/-/-/-/       -/
1101  TCAAAGGATC TTCTTGAGAT CCTTTTTGAT AATGGCCGGC CCCCCCCTT
      AGTTTCCTAG AAGAACTCTA GGAAAAACTA TTACCGGCCG GGGGGGGAA

      PacI
      -/-/-/
1151  AATTAAGGGG GGG
      TTAATTCCCC CCC
```

FIG. 35A-27
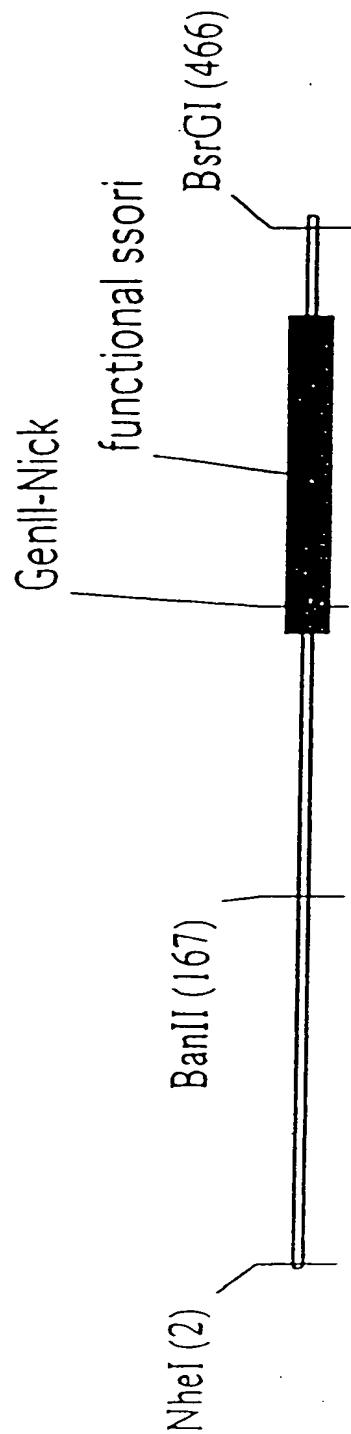
M11-11
470 bp
FIG. 35A-28

M11-II:

```
        NheI
        ------
  1   GCTAGCACGC GCCCTGTAGC GGCGCATTAA GCGCGGCGGG TGTGGTGGTT
      CGATCGTGCG CGGGACATCG CCGCGTAATT CGCGCCGCCC ACACCACCAA

 51   ACGCGCAGCG TGACCGCTAC ACTTGCCAGC GCCCTAGCGC CCGCTCCTTT
      TGCGCGTCGC ACTGGCGATG TGAACGGTCG CGGGATCGCG GGCGAGGAAA

101   CGCTTTCTTC CCTTCCTTTC TCGCCACGTT CGCCGGCTTT CCCCGTCAAG
      GCGAAAGAAG GGAAGGAAAG AGCGGTGCAA GCGGCCGAAA GGGGCAGTTC

        BanII
        -------
151   CTCTAAATCG GGGGCTCCCT TTAGGGTTCC GATTTAGTGC TTTACGGCAC
      GAGATTTAGC CCCCGAGGGA AATCCCAAGG CTAAATCACG AAATGCCGTG

201   CTCGACCCCA AAAAACTTGA TTAGGGTGAT GGTTCTCGTA GTGGGCCATC
      GAGCTGGGGT TTTTTGAACT AATCCCACTA CCAAGAGCAT CACCCGGTAG

251   GCCCTGATAG ACGGTTTTTC GCCCTTTGAC GTTGGAGTCC ACGTTCTTTA
      CGGGACTATC TGCCAAAAAG CGGGAAACTG CAACCTCAGG TGCAAGAAAT
```

FIG. 35A-29

301 ATAGTGGACT CTTGTTCCAA ACTGGAACAA CACTCAACCC TATCTCGGTC
      TATCACCTGA GAACAAGGTT TGACCTTGTT GTGAGTTGGG ATAGAGCCAG

351 TATTCTTTTG ATTTATAAGG GATTTTGCCG ATTTCGGCCT ATTGGTTAAA
      ATAAGAAAAC TAAATATTCC CTAAAACGGC TAAAGCCGGA TAACCAATTT

401 AAATGAGCTG ATTTAACAAA AATTTAACGC GAATTTTAAC AAAATATTAA
      TTTACTCGAC TAAATTGTTT TTAAATTGCG CTTAAAATTG TTTTATAATT

               BsrGI
               ~~~~~~

451 CGTTTACAAT TTCATGTACA
      GCAAATGTTA AAGTACATGT

FIG. 35A-30

FIG. 35A-31

M 12:

Bg1II
~~~~~~~
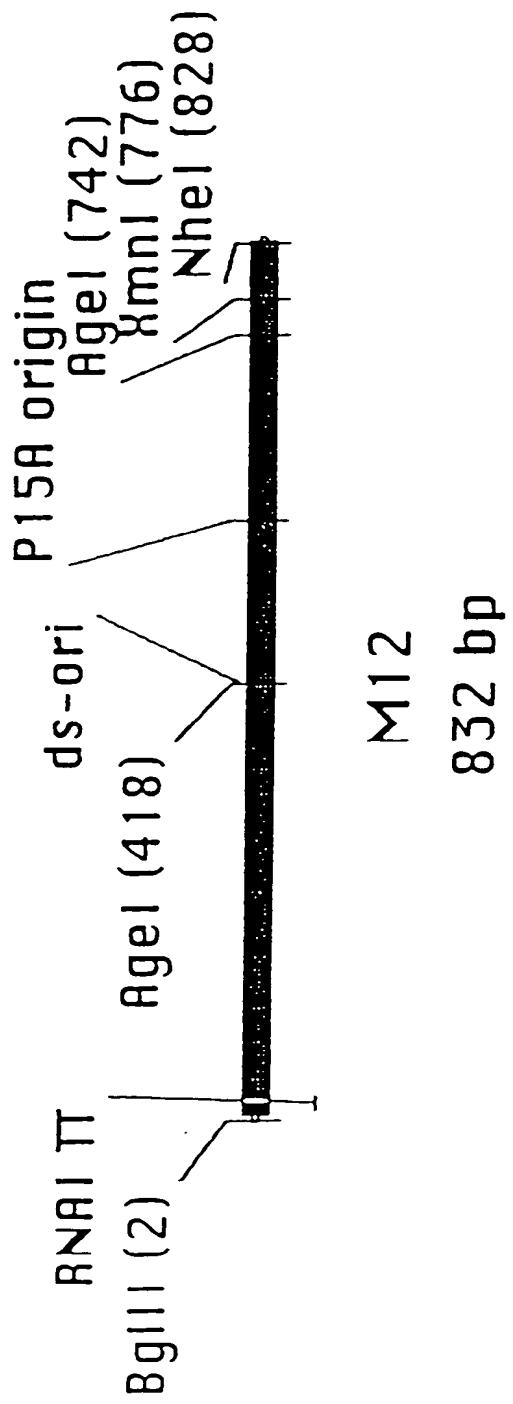
```
  1  AGATCTAATA  AGATGATCTT  CTTGAGATCG  TTTTGGTCTG  CGGGTAATCT
     TCTAGATTAT  TCTACTAGAA  GAACTCTAGC  AAAACCAGAC  GCGCATTAGA

 51  CTTGCTCTGA  AAACGAAAAA  ACCGCCTTGC  AGGGCGGGTT  TTCGTAGGTT
     GAACGAGACT  TTTGCTTTTT  TGGCGGAACG  TCCCGCCCAA  AAGCATCCAA

101  CTCTGAGCTA  CCAACTCTTT  GAACCGAGGT  AACTGGCTTG  GAGGAGCGCA
     GAGACTCGAT  GGTTGAGAAA  CTTGGCTCCA  TTGACCGAAC  CTCCTCGCGT

151  GTCACTAAAA  CTTGTCCTTT  CAGTTTAGCC  TTAACCGGCG  CATGACTTCA
     CAGTGATTTT  GAACAGGAAA  GTCAAATCGG  AATTGGCCGC  GTACTGAAGT

201  AGACTAACTC  CTCTAAATCA  ATTACCAGTG  GCTGCTGCCA  GTGGTGCTTT
     TCTGATTGAG  GAGATTTAGT  TAATGGTCAC  CGACGACGGT  CACCACGAAA

251  TGCATGTCTT  TCCGGGTTGG  ACTCAAGACG  ATAGTTACCG  GATAAGGCGC
     ACGTACAGAA  AGGCCCAACC  TGAGTTCTGC  TATCAATGGC  CTATTCCGCG

301  AGCGGGTCGGA  CTGAACGGGG  GGTTCGTGCA  TACAGTCCAG  CTTGGAGCGA
     TCGCCCAGCCT  GACTTGCCCC  CCAAGCACGT  ATGTCAGGTC  GAACCTCGCT
```

FIG. 35A-32

351 ACTGCCTACC CGGAACTGAG TGTCAGGCGT GGAATGAGAC AAACGCGGCC
     TGACGGATGG GCCTTGACTC ACAGTCCGCA CCTTACTCTG TTTGCGCCGG

                          Age I

401 ATAACAGCGG AATGACACCG GTAAACCGAA AGGCAGGAAC AGGAGAGCGC
     TATTGTCGCC TTACTGTGGC CATTTGGCTT TCCGTCCTTG TCCTCTCGCG

451 AGGAGGGAGC CGCCAGGGGG AAACGCCTGG TATCTTTATA GTCCTGTCGG
     TCCTCCCTCG GCGGTCCCCC TTTGCGGACC ATAGAAATAT CAGGACAGCC

501 GTTTCGCCAC CACTGATTTG AGCGGTCAGAT TTCGTGATGC TTGTCAGGGG
     CAAAGCGGTG GTGACTAAAC TCGCAGTCTA AAGCACTACG AACAGTCCCC

551 GGCGGAGCCT ATGGAAAAAC GGCTTTGCCG CGGCCCTCTC ACTTCCCTGT
     CCGCCTCGGA TACCTTTTTG CCGAAACGGC GCCGGGAGAG TGAAGGGACA

601 TAAGTATCTT CCTGGCATCT TCCAGGAAAT CTCCGCCCCG TTCGTAAGCC
     ATTCATAGAA GGACCGTAGA AGGTCCTTTA GAGGGCGGGC AAGCATTCGG

651 ATTTCCGCTC GCCGCAGTCG AACGACCGAG CGTAGCCGAGT CAGTGAGCGA
     TAAAGGCGAG CGGCGTCAGC TTGCTGGCTC GCATCGCTCA GTCACTCGCT

FIG. 35A-33

```
                                                        Age I
                                                        ~ ~ ~
701  GGAAGCGGAA  TATATCCTGT  ATCACATATT  CTGCTGACGC  ACCGGTGCAG
     CCTTCGCCTT  ATATAGGACA  TAGTGTATAA  GACGACTGCG  TGGCCACGTC

                              XmnI
                              ~ ~ ~ ~ ~
751  CCTTTTTCT   CCTGCCACAT  GAAGCACTTC  ACTGACACCC  TCATCAGTGC
     GGAAAAAGA   GGACGGTGTA  CTTCGTGAAG  TGACTGTGGG  AGTAGTCACG

                                          NheI
                                          ~ ~ ~ ~ ~
801  CAACATAGTA  AGCCAGTATA  CACTCCGCTA  GC
     GTTGTATCAT  TCGGTCATAT  GTGAGGCGAT  CG
```

FIG. 35A-34

BglII (2)

XmnI (39)

BglII (45)
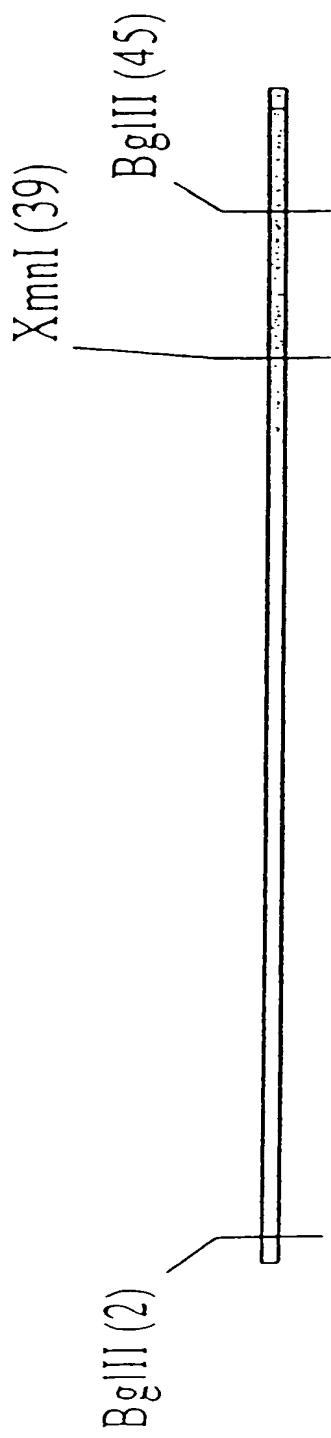
M13
49 bp

FIG. 35A-35

M 13:

```
        BglII                          XmnI         BglII
        - - - - -                      - - - - - - -   - 
1  AGATCTCATA ACTTCGTATA ATGTATGCTA TACGAAGTTA TTCAGATCT
   TCTAGAGTAT TGAAGCATAT TACATACGAT ATGCTTCAAT AAGTCTAGA
```

FIG. 35A-36
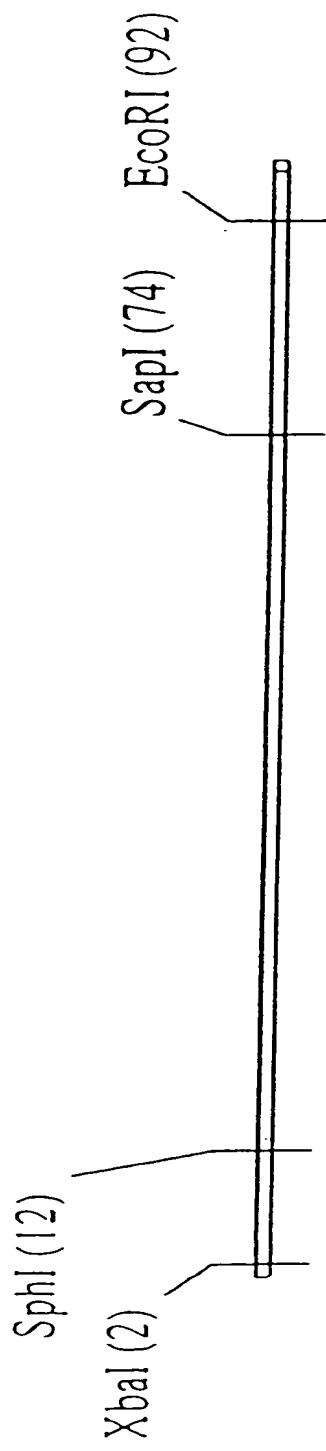
M19
96 bp

FIG. 35A-37

M 19:

```
              XbaI  SphI
              -      -----

    1   TCTAGAGCAT GCGTAGGAGA AAATAAAATG AAACAAAGCA CTATTGCACT
        AGATCTCGTA CGCATCCTCT TTTATTTTAC TTTGTTTCGT GATAACGTGA

                            SapI
                            -------

   51   GGCACTCTTA CCGTTGCTCT TCACCCCTGT TACCAAAGCC
        CCGTGAGAAT GGCAACGAGA AGTGGGGACA ATGGTTTCGG
```

EcoRI

GAATTC
CTTAAG
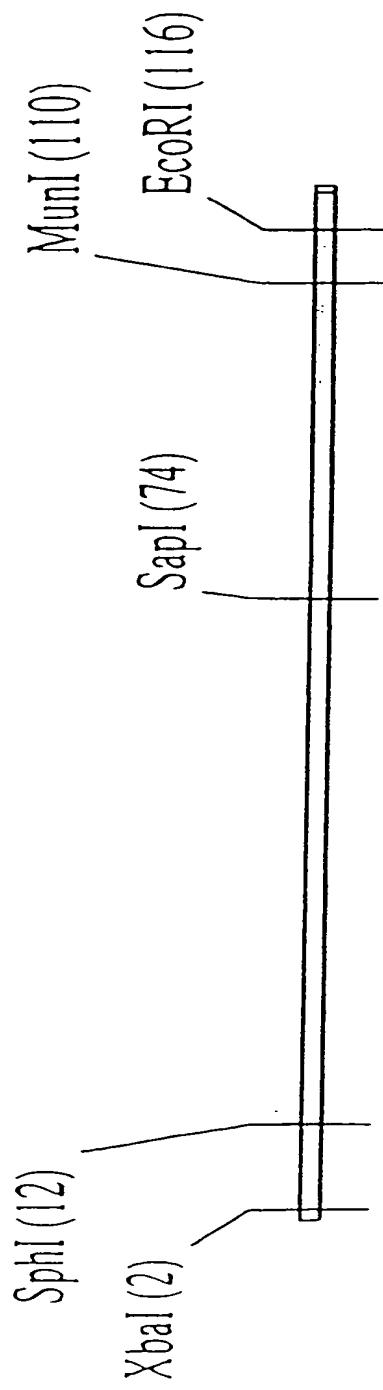
FIG. 35A-38

M20
120 bp

FIG. 35A-39

M 20:

```
      XbaI SphI
           ---------
1    TCTAGAGCAT GCGTAGGAGA AAATAAAATG AAACAAAGCA CTATTGCACT
     AGATCTCGTA CGCATCCTCT TTTATTTTAC TTTGTTTCGT GATAACGTGA

                       SapI
                       ---------
51   GGCACTCTTA CCGTTGCTCT TCACCCCTGT TACCAAAGCC GACTACAAAG
     CCGTGAGAAT GGCAACGAGA AGTGGGGACA ATGGTTTCGG CTGATGTTTC

          MunI EcoRI
               ---------
101  ATGAAGTGCA ATTGGAATTC
     TACTTCACGT TAACCTTAAG
```

FIG. 35A-40

NsiI (85)

EcoRI (92)

XbaI (2)
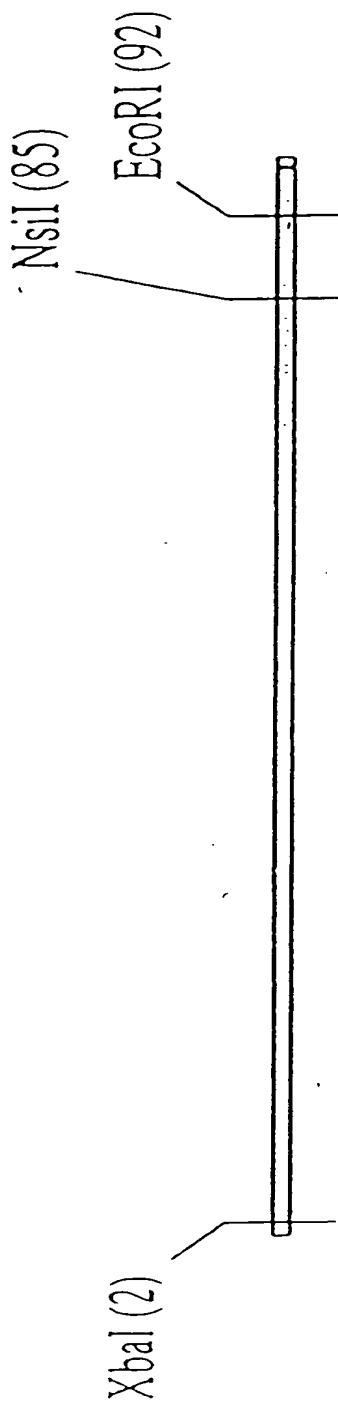
M21
96 bp

FIG. 35A-41

M 21:

```
      XbaI
      ------
1.    TCTAGAGGTT GAGGTGATTT TATGAAAAAG AATATCGCAT TTCTTCTTGC
      AGATCTCCAA CTCCACTAAA ATACTTTTTC TTATAGCGTA AAGAAGAACG

                              NsiI                  EcoRI
                              ------                ------
51.   ATCTATGTTC GTTTTTCTA TTGCTACAAA TGCATACGCT GAATTC
      TAGATACAAG CAAAAAAGAT AACGATGTTT ACGTATGCGA CTTAAG
```
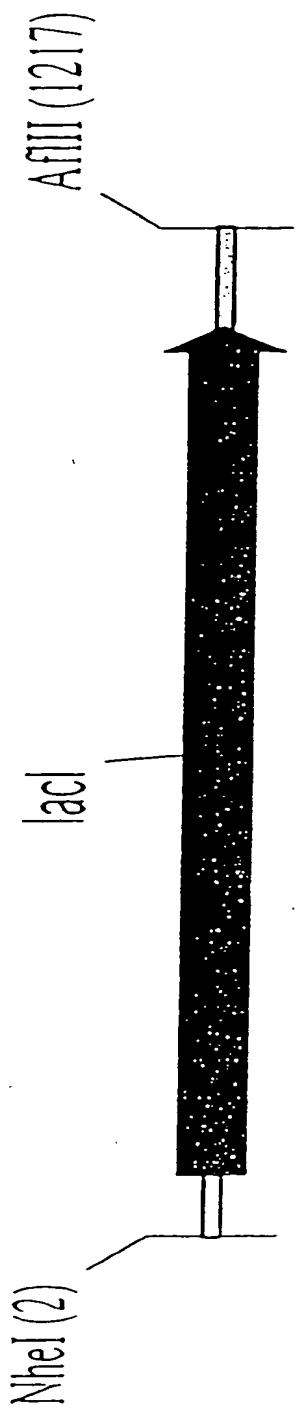
FIG. 35A-42

M41
1221 bp

FIG. 35A-43

M 41:

NheI
- - - -

1   GCTAGCATCG AATGGGCGCAA AACCTTTCGC GGTATGGCAT GATAGCGCCC
     CGATCGTAGC TTACCGCGTT TTGGAAAGCG CCATACCGTA CTATCGCGGG

51   GGAAGAGAGT CAATTCAGGG TGGTGAAATGT GAAACCAGTA ACGTTATACG
     CCTTCTCTCA GTTAAGTCCC ACCACTTACA CTTTGGTCAT TGCAATATGC

101 ATGTCGCAGA GTATGCCGGT GTCTCTTATC AGACCGTTTC CCGCGTGGTG
     TACAGCGTCT CATACGGCCA CAGAGAATAG TCTGGCAAAG GGCGCACCAC

151 AACCAGGCCA GCCACGTTTC TGCGAAAACG CGGGAAAAAG TGGAAGCGGC
     TTGGTCCGGT CGGTGCAAAG ACGCTTTTGC GCCCTTTTTC ACCTTCGCCG

201 GATGGCGGAG CTGAATTACA TTCCTAAACCG CGTGGCACAA CAACTGGCGG
     CTACCGCCTC GACTTAATGT AAGGATTGGC GCACCGTGTT GTTGACCGCC

251 GCAAACAGTC GGCGTTGCCA CCTCCAGTCT GGCCCTGCAC
     CGTTTGTCAG CCGCAACGGT GGAGGTCAGA CCGGGACGTG

301 GCGCCGTCGC AAATTGTCGC GGCGATTAAA TCTCGCGCCCG ATCAACTGGG
     CGCGGCAGCG TTTAACAGCG CCGCTAATTT AGAGCGCGGC TAGTTGACCC

FIG. 35A-44

```
351   TGCCAGCGTG GTCGTGTCGA TGGTAGAACG AAGCGGCGTC GAAGCCTGTA
      ACGGTCGCAC CAGCACAGCT ACCATCTTGC TTCGCCGCAG CTTCGGACAT

401   AAGCGGCGGT GCACAATCTT CTCGCGCAAC GTGTCAGTGG GCTGATTATT
      TTCGCCGCCA CGTGTTAGAA GAGCGCGTTG CACAGTCACC CGACTAATAA

451   AACTATCCGC TGGATGACCA GGATGCTATT GCTGTGGAAG CTGCCTGCAC
      TTGATAGGCG ACCTACTGGT CCTACGATAA CGACACCTTC GACGGACGTG

501   TAATGTTCCG GCGTTATTTC TTGATGTCTC TGACCAGACA CCCATCAACA
      ATTACAAGGC CGCAATAAAG AACTACAGAG ACTGGTCTGT GGGTAGTTGT

551   GTATTATTTT CTCCCATGAG GACGGTACGC GACTGGGCGT GGAGCATCTG
      CATAATAAAA GAGGGTACTC CTGCCATGCG CTGACCCGCA CCTCGTAGAC

601   GTCGCATTGG GCCACCAGCA AATCGCGCTG TTAGCTGGCC CATTAAGTTC
      CAGCGTAACC CGGTGGTCGT TTAGCGCGAC AATCGACCGG GTAATTCAAG

651   TGTCTCGGCG CGTCTGCGTC TGGCTGGCTG GCATAAATAT CTCACTCGCA
      ACAGAGCCGC GCAGACGCAG ACCGACGCAG CGTATTTATA GAGTGAGCGT

701   ATCAAATTCA GCCGATAGCG GAACGGGAAG GCGACTGGAG TGCCATGTCC
      TAGTTTAAGT CGGCTATCGC CTTGCCCTTC CGCTGACCTC ACGGTACAGG
```

FIG. 35A-45

```
 751  GGTTTTCAAC AAACCATGCA AATGCTGAAT GAGGGCATCG TTCCCACTGC
      CCAAAAGTTG TTTGGTACGT TTACGACTTA CTCCCGTAGC AAGGGTGACG

 801  GATGCTGGTT GCCAACGATC AGATGGCGCT GGGCGCAATG CGTGCCATTA
      CTACGACCAA CGGTTGCTAG TCTACCGCGA CCCGCGTTAC GCACGGTAAT

 851  CCGAGTCCGG GCTGCGCGTT GGTGCGGACA TCTCGGTAGT GGGATACGAC
      GGCTCAGGCC CGACGCGCAA CCACGCCTGT AGAGCCATCA CCCTATGCTG

 901  GATACCGAGG ACAGCTCATG TTATATCCCG CCGCTGACCA CCATCAAACA
      CTATGGCTCC TGTCGAGTAC AATATAGGGC GGCGACTGGT GGTAGTTTGT

 951  GGATTTTCGC CTGCTGGGGC AAACCAGCGT GGACCGCTTG CTGCAACTCT
      CCTAAAAGCG GACGACCCCG TTTGGTCGCA CCTGGCGAAC GACGTTGAGA

1001  CTCAGGGCCA GGCGGTGAAG GGCAATCAGC TGTTGCCCGT CTCACTGGTG
      GAGTCCCGGT CCGCCACTTC CCGTTAGTCG ACAACGGGCA GAGTGACCAC

1051  AAAAGAAAAA CCACCCTGGC TCCCAATACG CAAACCGCCT CTCCCCGCGC
      TTTTCTTTTT GGTGGGACCG AGGGTTATGC GTTTGGCGGA GAGGGGCGCG

1101  GTTGGCCGAT TCACTGATGC AGCTGGCACG ACAGGTTTCC CGACTGGAAA
      CAACCGGCTA AGTGACTACG TCGACCGTGC TGTCCAAAGG GCTGACCTTT
```

FIG. 35A-46

1151 GCGGGCAGTG AGGCTACCCG ATAAAAGCGG CTTCCTGACA GGAGGCCGTT
    CGCCCGTCAC TCCGATGGGC TATTTTCGCC GAAGGACTGT CCTCCGGCAA

          Aflii
          ~~~~~

1201 TTGTTTTGCA GCCCACTTAA G
    AACAAAACGT CGGGTGAATT C

FIG. 35A-47

FIG. 35A-48

```
pCAL0-1:
    BglII
    ~~~~~
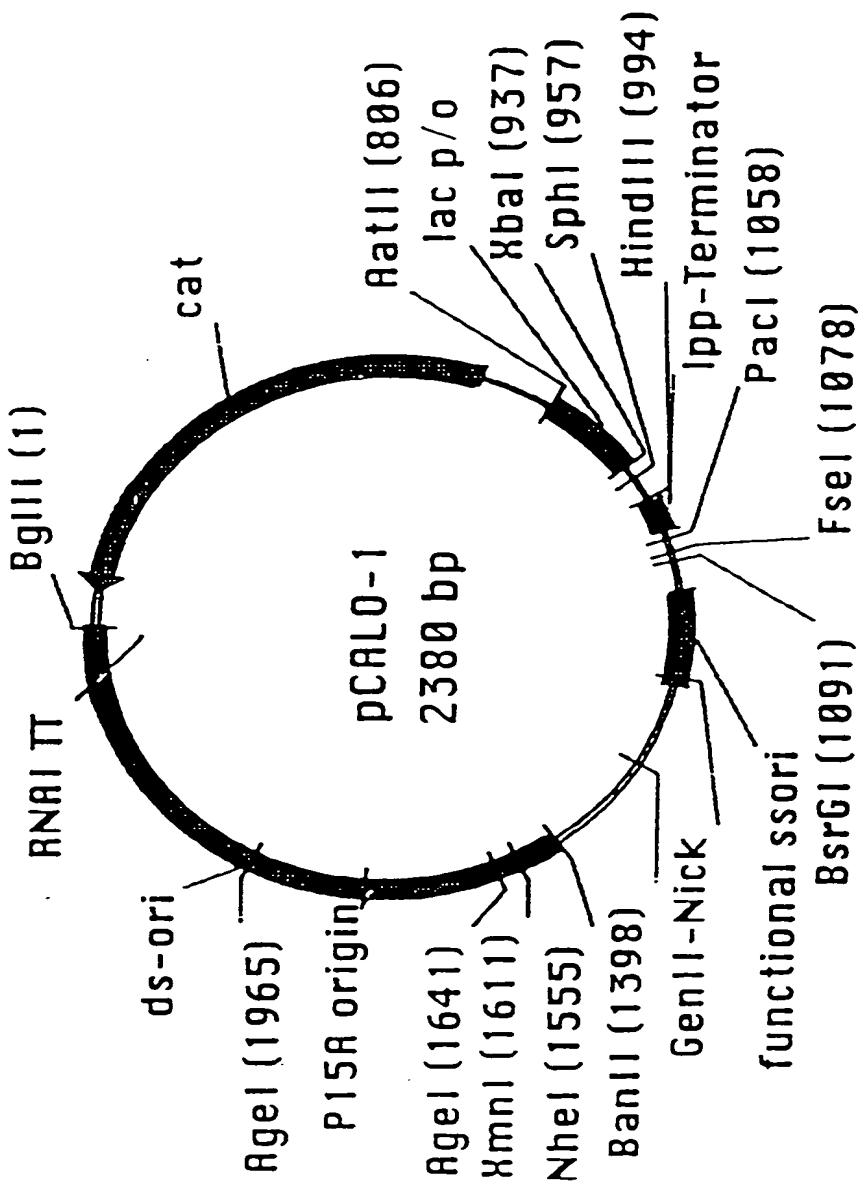
  1  GATCTAGCAC CAGGCGTTTA AGGGCACCAA TAACTGCCTT AAAAAAATTA
     CTAGATCGTG GTCCGCAAAT TCCCGTGGTT ATTGACGGAA TTTTTTTAAT

 51  CGCCCCGCCC TGCCACTCAT CGCAGTACTG TTGTAATTCA TTAAGCATTC
     GCGGGGCGGG ACGGTGAGTA GCGTCATGAC AACATTAAGT AATTCGTAAG

101  TGCCGACATG GAAGCCATCA CAAACGGCAT GATGAACCTG AATCGCCAGC
     ACGGCTGTAC CTTCGGTAGT GTTTGCCGTA CTACTTGGAC TTAGCGGGTCG

151  GGCATCAGCA CCTTGTCGCC TTGCGTATAA TATTTGCCCA TAGTGAAAAC
     CCGTAGTCGT GGAACAGCGG AACGCATATT ATAAACGGGT ATCACTTTTG

201  GGGGGCGAAG AAGTTGTCCA TATTGGCTAC GTTTAAATCA AAACTGGTGA
     CCCCCGCTTC TTCAACAGGT ATAACCGATG CAAATTTAGT TTTGACCACT

251  AACTCACCCA GGGATTGGCT GAGACGAAAA ACATATTCTC AATAAACCCT
     TTGAGTGGGT CCCTAACCGA CTCTGCTTTT TGTATAAGAG TTATTTGGGA

301  TTAGGGAAAT AGGCCAGGTT TTCACCGTAA CACGCCACAT CTTGCGAATA
     AATCCCTTTA TCCGGTCCAA AAGTGGCATT GTGCGGTGTA GAACGCTTAT
```

FIG. 35A-49

```
351  TATGTGTAGA AACTGCCGGA AATCGTCGTG GTATTCACTC CAGAGGGATG
     ATACACATCT TTGACGGCCT TTAGCAGCAC CATAAGTGAG GTCTCGCTAC

401  AAAACGTTTC AGTTTGCTCA TGGAAAACGG TGTAACAAGG GTGAACACTA
     TTTTGCAAAG TCAAACGAGT ACCTTTTGCC ACATTGTTCC CACTTGTGAT

451  TCCCATATCA CCAGCTCACC GTCTTTCATT GCCATACGGA ACTCCGGGTG
     AGGGTATAGT GGTCGAGTGG CAGAAAGTAA CGGTATGCCT TGAGGCCCAC

501  AGCATTCATC AGGCGGGCAA GAATGTGAAT AAAGGCCGGA TAAAACTTGT
     TCGTAAGTAG TCCGCCCGTT CTTACACTTA TTTCCGGCCT ATTTTGAACA

551  GCTTATTTTT CTTTACGGTC TTTAAAAAGG CCGTAATATC CAGCTGAACG
     CGAATAAAAA GAAATGCCAG AAATTTTTCC GGCATTATAG GTCGACTTGC

601  GTCTGGTTAT AGGTACATTG AGCAACTGAC TGAAATGCCT CAAAATGTTC
     CAGACCAATA TCCATGTAAC TCGTTGACTG ACTTTACGGA GTTTTACAAG

651  TTTACGATGC CATTGGGATA TATCAACGGT GGTATATCCA GTGATTTTTT
     AAATGCTACG GTAACCCTAT ATAGTTGCCA CCATATAGGT CACTAAAAAA

701  TCTCCATTTT AGCTTCCTTA GCTCCTGAAA ATCTCGATAA CTCAAAAAAT
     AGAGGTAAAA TCGAAGGAAT CGAGGACTTT TAGAGCTATT GAGTTTTTTA
```

FIG. 35A-50

```
751  ACGCCCGGTA GTGATCTTAT TTCATTATGG TGAAAGTTGG AACCTCACCC
     TGCGGGCCAT CACTAGAATA AAGTAATACC ACTTTCAACC TTGGAGTGGG
              AatII
              ~~~~~~

801  GACGTCTAAT GTGAGTTAGC TCACTCATTA GGCACCCCAG GCTTTACACT
     CTGCAGATTA CACTCAATCG AGTGAGTAAT CCGTGGGGTC CGAAATGTGA

851  TTATGCTTCC GGCTCGTATG TTGTGTGGAA TTGTGAGCGG ATAACAATTT
     AATACGAAGG CCGAGCATAC AACACACCTT AACACTCGCC TATTGTTAAA
                                          XbaI
                                          ~~~~~~~

901  CACACAGGAA ACAGCTATGA CCATGATTAC GAATTCCTAG ACCCCCCCC
     GTGTGTCCTT TGTCGATACT GGTACTAATG CTTAAAGATC TGGGGGGGGG

951  CGCATGCCAT AACTTCGTAT AATGTACGCT ATACGAAGTT ATAAGCTTGA
     GCGTACGGTA TTGAAGCATA TTACATGCGA TATGCTTCAA TATTCGAACT
       SphI                                       HindIII
       ~~~~~~                                      ~~~~~~

1001 CCTGTGAAGT GAAAAATGGC GCAGATTGTG CGACATTTTT TTTGTCTGCC
     GGACACTTCA CTTTTTACCG CGTCTAACAC GCTGTAAAAA AAACAGACGG
```

FIG. 35A-51

```
              PacI                    FseI                BsrGI
            ~~~~~~                  ~~~~~~~              ~~~~~~

1051   GTTTAATTAA  AGGGGGGGG  GGGCCGGCCT  GGGGGGGGT  GTACATGAAA
       CAAATTAATT  TCCCCCCCC  CCCGGCCGGA  CCCCCCCCA  CATGTACTTT

1101   TTGTAAACGT  TAATATTTTG  TTAAAATTCG  CGTTAAATTT  TTGTTAAATC
       AACATTTGCA  ATTATAAAAC  AATTTTAAGC  GCAATTTAAA  AACAATTTAG

1151   AGCTCATTTT  TTAACCAATA  GGCCGAAATC  GGCAAAATCC  CTTATAAATC
       TCGAGTAAAA  AATTGGTTAT  CCGGCTTTAG  CCGTTTTAGG  GAATATTTAG

1201   AAAAGAATAG  ACCGAGATAG  GGTTGAGTGT  TGTTCCAGTT  TGGAACAAGA
       TTTTCTTATC  TGGCTCTATC  CCAACTCACA  ACAAGGTCAA  ACCTTGTTCT

1251   GTCCACTATT  AAAGAACGTG  GACTCCAACG  TCAAAGGGCG  AAAAACCGTC
       CAGGTGATAA  TTTCTTGCAC  CTGAGGTTGC  AGTTTCCCGC  TTTTTGGCAG

1301   TATCAGGGCG  ATGGCCCACT  ACGAGAACCA  TCACCCTAAT  CAAGTTTTT
       ATAGTCCCGC  TACCGGGTGA  TGCTCTTGGT  AGTGGGATTA  GTTCAAAAAA

                                                       BanII
                                                     ~~~~~~
1351   GGGGTCGAGG  TGCCGTAAAG  CACTAAATCG  GAACCCTAAA  GGGAGCCCCC
       CCCCAGCTCC  ACGGCATTTC  GTGATTTAGC  CTTGGGATTT  CCCTCGGGGG
```

FIG. 35A-52

```
1401  GATTTAGAGC  TTGACGGGGA  AAGCCGGCGA  ACGTGGCGAG  AAAGGAAGGG
      CTAAATCTCG  AACTGCCCCT  TTCGGCCGCT  TGCACCGCTC  TTTCCTTCCC

1451  AAGAAAGCGA  AAGGAGCGGG  CGCTAGGGCG  CTGGCAAGTG  TAGCGGTCAC
      TTCTTTCGCT  TTCCTCGCCC  GCGATCCCGC  GACCGTTCAC  ATCGCCAGTG

1501  GCTGCGCGTA  ACCACCACAC  CCGCCGCGCT  TAATGCGCCG  CTACAGGGCG
      CGACGCGCAT  TGGTGGTGTG  GGCGGCGCGA  ATTACGCGGC  GATGTCCCGC

                  NheI

1551  CGTGCTAGCG  GAGTGTATAC  TGGCTTACTA  TGTTGGCACT  GATGAGGGTG
      GCACGATCGC  CTCACATATG  ACCGAATGAT  ACAACCGTGA  CTACTCCCAC

                              XmnI                    AgeI

1601  TCAGTGAAGT  GCTTCATGTG  GCAGGAGAAA  AAAGGCTGCA  CCGGTGCGTC
      AGTCACTTCA  CGAAGTACAC  CGTCCTCTTT  TTTCCGACGT  GGCCACGCAG

1651  AGCAGAATAT  GTGATACAGG  ATATATTCCG  CTTCCTCGCT  CACTGACTCG
      TCGTCTTATA  CACTATGTCC  TATATAAGGC  GAAGGAGCGA  GTGACTGAGC

1701  CTACGCTCGG  TCGTTCGACT  GCGGCGAGCG  GAAATGGCTT  ACGAACGGGG
```

FIG. 35A-53

```
      GATGCCGAGCC AGCAAGCTGA CGCCGCTCGC CTTTACCGAA TGCTTGCCCC

1751  CGGAGATTTC CTGGAAGATG CCAGGAAGAT ACTTAACAGG GAAGTGAGAG
      GCCTCTAAAG GACCTTCTAC GGTCCTTCTA TGAATTGTCC CTTCACTCTC

1801  GGCCGCGGCA AAGCCGTTTT TCCATAGGCT CCGCCCCCCT GACAAGCATC
      CCGGCGCCGT TTCGGCAAAA AGGTATCCGA GGCGGGGGGA CTGTTCGTAG

1851  ACGAAATCTG ACGCTCAAAT CAGTGGTGGC GAAACCCGAC AGGACTATAA
      TGCTTTAGAC TGCGAGTTTA GTCACCACCG CTTTGGGCTG TCCTGATATT

1901  AGATACCAGG CGTTTCCCCC TGGCGGCTCC CTCCTGCGCT CTCCTGTTCC
      TCTATGGTCC GCAAAGGGGG ACCGCCGAGG GAGGACGCGA GAGGACAAGG

                           AgeI
                           ~~~~~~

1951  TGCCTTTCGG TTTACCGGTG TCATTCCGCT GTTATGGCCG CGTTTGTCTC
      ACGGAAAGCC AAATGGCCAC AGTAAGGCGA CAATACCGGC GCAAACAGAG

2001  ATTCCACGCC TGACACTCAG TTCCGGGTAG GCAGTTCGCT CCAAGCTGGA
      TAAGGTGCGG ACTGTGAGTC AAGGCCCATC CGTCAAGCGA GGTTCGACCT

2051  CTGTATGCAC GAACCCCCCG TTCAGTCCGA CCGCTGCGCC TTATCCGGTA
      GACATACGTG CTTGGGGGGC AAGTCAGGCT GGCGACGCGG AATAGGCCAT
```

FIG. 35A-54

```
2101  ACTATCGTCT  TGAGTCCAAC  CCGGAAAGAC  ATGCAAAAGC  ACCACTGGCA
      TGATAGCAGA  ACTCAGGTTG  GGCCTTTCTG  TACGTTTTCG  TGGTGACCGT

2151  GCAGCCACTG  GTAATTGATT  TAGAGGAGTT  AGTCTTGAAG  TCATGCGCCG
      CGTCGGTGAC  CATTAACTAA  ATCTCCTCAA  TCAGAACTTC  AGTACGCGGC

2201  GTTAAGGCTA  AACTGAAAGG  ACAAGTTTTA  GTGACTGCGC  TCCTCCAAGC
      CAATTCCGAT  TTGACTTTCC  TGTTCAAAAT  CACTGACGCG  AGGAGGTTCG

2251  CAGTTACCTC  GGTTCAAAGA  GTTGGTAGCT  CAGAGAACCT  ACGAAAAACC
      GTCAATGGAG  CCAAGTTTCT  CAACCATCGA  GTCTCTTGGA  TGCTTTTTGG

2301  GCCCTGCAAG  GCGGTTTTTT  CGTTTTCAGA  GCAAGAGATT  ACGGCGCAGAC
      CGGGACGTTC  CGCCAAAAAA  GCAAAAGTCT  CGTTCTCTAA  TGCGCGTCTG

                              Bg1II
                              ~

2351  CAAAACGATC  TCAAGAAGAT  CATCTTATTA
      GTTTTGCTAG  AGTTCTTCTA  GTAGAATAAT
```

FIG. 35A-55

FIG. 35A-56

pCAL0-2:

BsrGI
~~~~~

```
1    GTACATGAAA TTGTAAACGT TAATATTTTG TTAAAATTCG CGTTAAATTT
     CATGTACTTT AACATTTGCA ATTATAAAAC AATTTTAAGC GCAATTTAAA

51   TTGTTAAATC AGCTCATTTT TTAACCAATA GGCCGAAATC GGCAAAATCC
     AACAATTTAG TCGAGTAAAA AATTGGTTAT CCGGCTTTAG CCGTTTTAGG

101  CTTATAAATC AAAAGAATAG ACCGAGATAG GGTTGAGTGT TGTTCCAGTT
     GAATATTTAG TTTTCTTATC TGGCTCTATC CCAACTCACA ACAAGGTCAA

151  TGGAACAAGA GTCCACTATT AAAGAACGTG GACTCCAACG TCAAAGGGCG
     ACCTTGTTCT CAGGTGATAA TTTCTTGCAC CTGAGGTTGC AGTTTCCCGC

201  AAAAACCGTC TATCAGGGCG ATGGCCCACT ACGAGAACCA TCACCCTAAT
     TTTTTGGCAG ATAGTCCCGC TACCGGGTGA TGCTCTTGGT AGTGGGATTA

251  CAAGTTTTTT GGGGTCGAGG TGCCGTAAAG CACTAAATCG GAACCCTAAA
     GTTCAAAAAA CCCCAGCTCC ACGGCATTTC GTGATTTAGC CTTGGGATTT

          BanII
          ~~~~~
301  GGGAGCCCCC GATTTAGAGC TTGACGGGGA AAGCCGGCGA ACGTGGCGAG
```

FIG. 35A-57

```
          CCCTCGGGGG  CTAAATCTCG  AACTGCCCCT  TTCGGCCGCT  TGCACCGCTC

  351

          AAAGGAAGGG  AAGAAAGCGA  AAGGAGCGGG  CGCTAGGGCG  CTGGCAAGTG
          TTTCCTTCCC  TTCTTTCGCT  TTCCTCGCCC  GCGATCCCGC  GACCGTTCAC

  401

          TAGCGGTCAC  GCTGCGCGTA  ACCACCACAC  CCGCCGCGCT  TAATGCGCCG
          ATCGCCAGTG  CGACGCGCAT  TGGTGGTGTG  GGCGGCGCGA  ATTACGCGGC
                                              NheI
                                              ~~~~

          CTACAGGGCG  CGTGCTAGCG  GAGTGTATAC  TGGCTTACTA  TGTTGGCACT
  451     GATGTCCCGC  GCACGATCGC  CTCACATATG  ACCGAATGAT  ACAACCGTGA
                                  XmnI                    AgeI
                                  ~~~~~~~~~~              ~

          GATGAGGGTG  TCAGTGAAGT  GCTTCATGTG  GCAGGAGAAA  AAAGGCTGCA
  501     CTACTCCCAC  AGTCACTTCA  CGAAGTACAC  CGTCCTCTTT  TTTCCGACGT
          AgeI
          ~~~~~

          CCGGTGCGTC  AGCAGAATAT  GTGATACAGG  ATATATTCCG  CTTCCTCGCT
  551     GGCCACGCAG  TCGTCTTATA  CACTATGTCC  TATATAAGGC  GAAGGAGCGA

  601     CACTGACTCG  CTACGCTCGG  TCGTTCGACT  GCGGGCGAGCG  GAAATGGCTT
```

FIG. 35A-58

```
      GTGACTGAGC GATGCGAGCC AGCAAGCTGA CGCCGCTCGC CTTTACCGAA

651   ACGAACGGGG CGGAGATTTC CTGGAAGATG CCAGGAAGAT ACTTAACAGG
      TGCTTGCCCC GCCTCTAAAG GACCTTCTAC GGTCCTTCTA TGAATTGTCC

701   GAAGTGAGAG GGCCGCGGCA AAGCCGTTTT TCCATAGGCT CCGCCCCCCT
      CTTCACTCTC CCGGCGCCGT TTCGGCAAAA AGGTATCCGA GGCGGGGGGA

751   GACAAGCATC ACGAAATCTG ACGCTCAAAT CAGTGGTGGC GAAACCCGAC
      CTGTTCGTAG TGCTTTAGAC TGCGAGTTTA GTCACCACCG CTTTGGGCTG

801   AGGACTATAA AGATACCAGG CGTTTCCCCC TGGCGGCTCC CTCCTGCGCT
      TCCTGATATT TCTATGGTCC GCAAAGGGGG ACCGCCGAGG GAGGACGCGA
                                     AgeI
                                     ~~~~~

851   CTCCTGTTCC TGCCTTTCGG TTTACCGGTG TCATTCCGCT GTTATGGCCG
      GAGGACAAGG ACGGAAAGCC AAATGGCCAC AGTAAGGCGA CAATACCGGC

901   CGTTTGTCTC ATTCCACGCC TGACACTCAG TTCCGGGTAG GCAGTTCGCT
      GCAAACAGAG TAAGGTGCGG ACTGTGAGTC AAGGCCCATC CGTCAAGCGA

951   CCAAGCTGGA CTGTATGCAC GAACCCCCCG TTCAGTCCGA CCGCTGCGCC
      GGTTCGACCT GACATACGTG CTTGGGGGGC AAGTCAGGCT GGCGAGCGGG
```

FIG. 35A-59

```
1001  TTATCCGGTA ACTATCGTCT TGAGTCCAAC CCGGAAAGAC ATGCAAAAGC
      AATAGGCCAT TGATAGCAGA ACTCAGGTTG GGCCTTTCTG TACGTTTTCG

1051  ACCACTGGCA GCAGCCACTG GTAATTGATT TAGAGGAGTT AGTCTTGAAG
      TGGTGACCGT CGTCGGTGAC CATTAACTAA ATCTCCTCAA TCAGAACTTC

1101  TCATGCGCCG GTTAAGGCTA AACTGAAAGG ACAAGTTTTA GTGACTGCGC
      AGTACGCGGC CAATTCCGAT TTGACTTTCC TGTTCAAAAT CACTGACGCG

1151  TCCTCCAAGC CAGTTACCTC GGTTCAAAGA GTTGGTAGCT CAGAGAACCT
      AGGAGGTTCG GTCAATGGAG CCAAGTTTCT CAACCATCGA GTCTCTTGGA

1201  ACGAAAAACC GCCCTGCAAG GCGGTTTTTT CGTTTTCAGA GCAAGAGATT
      TGCTTTTTGG CGGGACGTTC CGCCAAAAAA GCAAAAGTCT CGTTCTCTAA

                                                  Bgl II
                                                  ~~~~~~~

1251  ACGCGCAGAC CAAAACGATC TCAAGAAGAT CATCTTATTA GATCTAGCAC
      TGCGCGTCTG GTTTTGCTAG AGTTCTTCTA GTAGAATAAT CTAGATCGTG

1301  CAGGCGTTTA AGGGCACCAA TAACTGCCTT AAAAAAATTA CGCCCCGCCC
      GTCCGCAAAT TCCCGTGGTT ATTGACGGAA TTTTTTTAAT GCGGGGCGGG
```

FIG. 35A-60

```
1351   TGCCACTCAT CGCAGTACTG TTGTAATTCA TTAAGCATTC TGCCGACATG
       ACGGTGAGTA GCGTCATGAC AACATTAAGT AATTCGTAAG ACGGCTGTAC

1401   GAAGCCATCA CAAACGGCAT GATGAACCTG AATCGCCAGC GGCATCAGCA
       CTTCGGTAGT GTTTGCCGTA CTACTTGGAC TTAGCGGTCG CCGTAGTCGT

1451   CCTTGTCGCC TTGCGTATAA TATTTGCCCA TAGTGAAAAC GGGGGCGAAG
       GGAACAGCGG AACGCATATT ATAAACGGGT ATCACTTTTG CCCCCGCTTC

1501   AAGTTGTCCA TATTGGCTAC GTTTAAATCA AAACTGGTGA AACTCACCCA
       TTCAACAGGT ATAACCGATG CAAATTTAGT TTTGACCACT TTGAGTGGGT

1551   GGGATTGGCT GAGACGAAAA ACATATTCTC AATAAACCCT TTAGGGAAAT
       CCCTAACCGA CTCTGCTTTT TGTATAAGAG TTATTTGGGA AATCCCTTTA

1601   AGGCCAGGTT TTCACCGTAA CACGCCACAT CTTGCGAATA TATGTGTAGA
       TCCGGTCCAA AAGTGGCATT GTGCGGTGTA GAACGCTTAT ATACACATCT

1651   AACTGCCGGA AATCGTCGTG GTATTCACTC CAGAGGCGATG AAAACGTTTC
       TTGACGGCCT TTAGCAGCAC CATAAGTGAG GTCTCGCTAC TTTGCAAAG

1701   AGTTTGCTCA TGGAAAACGG TGTAACAAGG GTGAACACTA TCCCATATCA
       TCAAACGAGT ACCTTTTGCC ACATTGTTCC CACTTGTGAT AGGGTATAGT
```

FIG. 35A-61

```
1751  CCAGCTCACC GTCTTTCATT GCCATACGGA ACTCCGGGTG AGCATTCATC
      GGTCGAGTGG CAGAAAGTAA CGGTATGCCT TGAGGCCCAC TCGTAAGTAG

1801  AGGCGGGCAA GAATGTGAAT AAAGGCCGGA TAAAACTTGT GCTTATTTTT
      TCCGCCCGTT CTTACACTTA TTTCCGGCCT ATTTTGAACA CGAATAAAAA

1851  CTTTACGGTC TTTAAAAAGG CCGTAATATC CAGCTGAACG GTCTGGTTAT
      GAAATGCCAG AAATTTTTCC GGCATTATAG GTCGACTTGC CAGACCAATA

1901  AGGTACATTG AGCAACTGAC TGAAATGCCT CAAAATGTTC TTTACGATGC
      TCCATGTAAC TCGTTGACTG ACTTTACGGA GTTTTACAAG AAATGCTACG

1951  CATTGGGATA TATCAACGGT GGTATATCCA GTGATTTTTT TCTCCATTTT
      GTAACCCTAT ATAGTTGCCA CCATATAGGT CACTAAAAAA AGAGGTAAAA

2001  AGCTTCCTTA GCTCCTGAAA ATCTCGATAA CTCAAAAAAT ACGCCCGGTA
      TCGAAGGAAT CGAGGACTTT TAGAGCTATT GAGTTTTTTA TGCGGGCCAT

                                                AatII
                                                ~~~~~~
2051  GTGATCTTAT TTCATTATGG TGAAAGTTGG AACCTCACCC GACGTCTAAT
      CACTAGAATA AAGTAATACC ACTTTCAACC TTGGAGTGGG CTGCAGATTA

2101  GTGAGTTAGC TCACTCATTA GGCACCCCAG GCTTTACACT TTATGCTTCC
```

FIG. 35A-62

```
      CACTCAATCG AGTGAGTAAT CCGTGGGGTC CGAAATGTGA AATACGAAGG

                                                     SphI
                                                   ~~~~~~
2151  GGCTCGTATG TTGTGTGGAA ATAACAATTT CACACAGGAA
      CCGAGCATAC AACACACCTT TATTGTTAAA GTGTGTCCTT

                 XbaI                          SphI
               ~~~~~~                        ~~~~~~
2201  ACAGCTATGA CCATGATTAC GAATTTCTAG ACCCCCCCCC CGCATGCCAT
      TGTCGATACT GGTACTAATG CTTAAAGATC TGGGGGGGGG GCGTACGGTA

                              HindIII
                            ~~~~~~
2251  AACTTCGTAT AATGTACGCT ATACGAAGTT ATAAGCTTGA CCTGTGAAGT
      TTGAAGCATA TTACATGCGA TATGCTTCAA TATTCGAACT GGACACTTCA

                                                  PacI
                                               ~~~~~~
2301  GAAAAATGGC GCAGATTGTG CGACATTTTT TTTGTCTGCC GTTTAATTAA
      CTTTTTACCG CGTCTAACAC GCTGTAAAAA AAACAGACGG CAAATTAATT

          FseI
       ~~~~~~~~
2351  GGGGGGGGGC CGGCCATTAT CAAAAAGGAT CTCAAGAAGA TCCTTTGATC
      CCCCCCCCCG GCCGGTAATA GTTTTTCCTA GAGTTCTTCT AGGAAACTAG
```

FIG. 35A-63

```
2401   TTTTCTACGG GGTCTGACGC TCAGTGGAAC GAAAACTCAC GTTAAGGGAT
       AAAAGATGCC CCAGACTGCG AGTCACCTTG CTTTTGAGTG CAATTCCCTA

2451   TTTGGTCATG AGATTATCAA AAAGGATCTT CACCTAGATC CTTTTAAATT
       AAACCAGTAC TCTAATAGTT TTTCCTAGAA GTGGATCTAG GAAAATTTAA

2501   AAAAATGAAG TTTTAAATCA ATCTAAAGTA TATATGAGTA AACTTGGTCT
       TTTTTACTTC AAAATTTAGT TAGATTTCAT ATATACTCAT TTGAACCAGA

2551   GACAGTTACC CAATGCTTAA TCAGTGAGGC ACCTATCTCA GCGATCTGTC
       CTGTCAATGG GTTACGAATT AGTCACTCCG TGGATAGAGT CGCTAGACAG

2601   TATTTCGTTC ATCCATAGTT GCCTGACTCC CCGTCGTGTA GATAACTACG
       ATAAAGCAAG TAGGTATCAA CGGACTGAGG GGCAGCACAT CTATTGATGC

2651   ATACGGGAGG GCTTACCATC TGGCCCCAGT GCTGCAATGA TACCGCGAGA
       TATGCCCTCC CGAATGGTAG ACCGGGGTCA CGACGTTACT ATGGCGCTCT

2701   CCCACGCTCA CCGGCTCCAG ATTTATCAGC AATAAACCAG CCAGCCGGAA
       GGGTGCGAGT GGCCGAGGTC TAAATAGTCG TTATTTGGTC GGTCGGCCTT

2751   GGGCCGAGCG CAGAAGTGGT CCTGCAACTT TATCCGCCTC CATCCAGTCT
       CCCGGCTCGC GTCTTCACCA GGACGTTGAA ATAGGCGGAG GTAGGTCAGA
```

FIG. 35A-64

```
2801   ATTAACTGTT  GCCGGGAAGC  TAGAGTAAGT  AGTTCGCCAG  TTAATAGTTT
       TAATTGACAA  CGGCCCTTCG  ATCTCATTCA  TCAAGCGGTC  AATTATCAAA

2851   GCGCAACGTT  GTTGCCATTG  CTACAGGCAT  CGTGGTGTCA  CGCTCGTCGT
       CGCGTTGCAA  CAACGGTAAC  GATGTCCGTA  GCACCACAGT  GCGAGCAGCA

2901   TTGGTATGGC  TTCATTCAGC  TCCGGTTCCC  AACGATCAAG  GCGAGTTACA
       AACCATACCG  AAGTAAGTCG  AGGCCAAGGG  TTGCTAGTTC  CGCTCAATGT

2951   TGATCCCCCA  AAAAGCGGTT  AGCTCCTTCG  GTCCTCCGAT
       ACTAGGGGGT  ACAACACGTT  TTTTCGCCAA  TCGAGGAAGC  CAGGAGGCTA

3001   CGTTGTCAGA  AGTAAGTTGG  CCGCAGTGTT  ATCACTCATG  GTTATGGCAG
       GCAACAGTCT  TCATTCAACC  GGCGTCACAA  TAGTGAGTAC  CAATACCGTC

3051   CACTGCATAA  TTCTCTTACT  GTCATGCCAT  CCGTAAGATG  CTTTTCTGTG
       GTGACGTATT  AAGAGAATGA  CAGTACGGTA  GGCATTCTAC  GAAAAGACAC

3101   ACTGGTGAGT  ACTCAACCAA  GTCATTCTGA  GAATAGTGTA  TGCGGCGACC
       TGACCACTCA  TGAGTTGGTT  CAGTAAGACT  CTTATCACAT  ACGCCGCTGG

3151   GAGTTGCTCT  TGCCCGGCGT  CAATACGGGA  TAATACCGCG  CCACATAGCA
       CTCAACGAGA  ACGGGCCGCA  GTTATGCCCT  ATTATGGCGC  GGTGTATCGT
```

FIG. 35A-65

XmnI

```
3201  GAACTTTAAA AGTGCTCATC ATTGGAAAAC GTTCTTCGGG GCGAAAACTC
      CTTGAAATTT TCACGAGTAG TAACCTTTTG CAAGAAGCCC CGCTTTTGAG

3251  TCAAGGATCT TACCGCTGTT GAGATCCAGT TCGATGTAAC CCACTCGCGC
      AGTTCCTAGA ATGGCGACAA CTCTAGGTCA AGCTACATTG GGTGAGCGCG

3301  ACCCAACTGA TCCTCAGCAT CTTTTACTTT CACCAGCGTT TCTGGGTGAG
      TGGGTTGACT AGGAGTCGTA GAAAATGAAA GTGGTCGCAA AGACCCACTC

3351  CAAAAACAGG AAGGCAAAAT GCCGCAAAAA AGGGAATAAG GGCGACACGG
      GTTTTTGTCC TTCCGTTTTA CGGCGTTTTT TCCCTTATTC CCGCTGTGCC

3401  AAATGTTGAA TACTCATACT CTTCCTTTTT CAATATTATT GAAGCATTTA
      TTTACAACTT ATGAGTATGA GAAGGAAAAA GTTATAATAA CTTCGTAAAT
```

BsrGI

```
3451  TCAGGGTTAT TGTCTCATGA GCGGATACAT ATTTGAAT
      AGTCCCAATA ACAGAGTACT CGCCTATGTA TAAACTTA
```

FIG. 35A-66

FIG. 35A-67

pCALO-3:

```
        BglII
        ~~~~~

  1     GATCTCATAA  CTTCGTATAA  TGTATGCTAT  ACGAAGTTAT
        CTAGAGTATT  GAAGCATATT  ACATACGATA  TGCTTCAATA

 51     GTGAGTTAGC  TCACTCATTA  GGCACCCCAG  GCTTTACACT
        CACTCAATCG  AGTGAGTAAT  CCGTGGGGTC  CGAAATGTGA

101     GGCTCGTATG  TTGTGTGGAA  TTGTGAGCGG  ATAACAATTT
        CCGAGCATAC  AACACACCTT  AACACTCGCC  TATTGTTAAA

                    XbaI
                    ~~~~~
                    ~

151     ACAGCTATGA  CCATGATTAC  GAATTTCTAG  ACCCCCCCCC
        TGTCGATACT  GGTACTAATG  CTTAAAGATC  TGGGGGGGGG

                        HindIII
                        ~~~~~

201     AACTTCGTAT  AATGTACGCT  ATACGAAGTT  ATAAGCTTGA
        TTGAAGCATA  TTACATGCGA  TATGCTTCAA  TATTCGAACT
```

```
                                    AatII
                                    ~~~~~~~

                                    GACGTCTAAT
                                    CTGCAGATTA

                                    TTATGCTTCC
                                    AATACGAAGG

                                    CACACAGGAA
                                    GTGTGTCCTT

                        SphI
                        ~~~~~~
                        ~

                        CGCATGCCAT
                        GCGTACGGTA

                                    CCTGTGAAGT
                                    GGACACTTCA

                                    PacI
```

FIG. 35A-68

```
251  GAAAAATGGC  GCAGATTGTG  CGACATTTTT  TTTGTCTGCC  GTTTAATTAA
     CTTTTTACCG  CGTCTAACAC  GCTGTAAAAA  AAACAGACGG  CAAATTAATT

                  FseI

301  GGGGGGGGGC  CGGCCATTAT  CAAAAAGGAT  CTCAAGAAGA  TCCTTTGATC
     CCCCCCCCCG  GCCGGTAATA  GTTTTTCCTA  GAGTTCTTCT  AGGAAACTAG

351  TTTTCTACGG  GGTCTGACGC  TCAGTGGAAC  GAAAACTCAC  GTTAAGGAT
     AAAAGATGCC  CCAGACTGCG  AGTCACCTTG  CTTTTGAGTG  CAATTCCCTA

401  TTTGGTCATG  AGATTATCAA  AAAGGATCTT  CACCTAGATC  CTTTTAAATT
     AAACCAGTAC  TCTAATAGTT  TTTCCTAGAA  GTGGATCTAG  GAAAATTTAA

451  AAAAATGAAG  TTTTAAATCA  ATCTAAAGTA  TATATGAGTA  AACTTGGTCT
     TTTTTACTTC  AAAATTTAGT  TAGATTTCAT  ATATACTCAT  TTGAACCAGA

501  GACAGTTACC  CAATGCTTAA  TCAGTGAGGC  ACCTATCTCA  GCGATCTGTC
     CTGTCAATGG  GTTACGAATT  AGTCACTCCG  TGGATAGAGT  CGCTAGACAG

551  TATTTCGTTC  ATCCATAGTT  GCCTGACTCC  CCGTCGTGTA  GATAACTACG
     ATAAAGCAAG  TAGGTATCAA  CGGACTGAGG  GGCAGCACAT  CTATTGATGC
```

FIG. 35A-69

```
601   ATACGGGAGG GCTTACCATC TGGCCCCAGT GCTGCAATGA TACCGGGAGA
      TATGCCCTCC CGAATGGTAG ACCGGGGTCA CGACGTTACT ATGGGCCTCT

651   CCACGCTCA  CCGGCTCCAG ATTTATCAGC AATAAACCAG CCAGCCGGAA
      GGGTGCGAGT GGCCGAGGTC TAAAATAGTCG TTATTTGGTC GGTCGGCCTT

701   GGGCCGAGCG CAGAAGTGGT CCTGCAACTT TATCCGCCTC CATCCAGTCT
      CCCGGCTCGC GTCTTCACCA GGACGTTGAA ATAGGCGGAG GTAGGTCAGA

751   ATTAAACTGTT GCCGGGAAGC TAGAGTAAGT AGTTCGCCAG TTAATAGTTT
      TAATTGACAA CGGCCCTTCG ATCTCATTCA TCAAGCGGTC AATTATCAAA

801   GCGCAACGTT GTTGCCATTG CTACAGGCAT CGTGGTGTCA CGCTCGTCGT
      CGCGTTGCAA CAACGGTAAC GATGTCCGTA GCACCACAGT GCGAGCAGCA

851   TTGGTATGGC TTCATTCAGC TCCGGTTCCC AACGATCAAG GCGAGTTACA
      AACCATACCG AAGTAAGTCG AGGCCAAGGG TTGCTAGTTC CGCTCAATGT

901   TGATCCCCCA TGTTGTGCAA AAAAGCGGTT AGCTCCTTCG GTCCTCCGAT
      ACTAGGGGGT ACAACACGTT TTTTCGCCAA TCGAGGAAGC CAGGAGGCTA

951   CGTTGTCAGA AGTAAGTTGG CCGCAGTGTT ATCACTCATG GTTATGGCAG
      GCAACAGTCT TCATTCAACC GGCGTCACAA TAGTGAGTAC CAATACCGTC
```

FIG. 35A-70

```
1001   CACTGCATAA   TTCTCTTACT   GTCATGCCAT   CCGTAAGATG   CTTTTCTGTG
       GTGACGTATT   AAGAGAATGA   CAGTACGGTA   GGCATTCTAC   GAAAAGACAC

1051   ACTGGTGAGT   ACTCAACCAA   GTCATTCTGA   GAATAGTGTA   TGCGGCGACC
       TGACCACTCA   TGAGTTGGTT   CAGTAAGACT   CTTATCACAT   ACGCCGCTGG

1101   GAGTTGCTCT   TGCCCGGCGT   CAATACGGGA   TAATACCGCG   CCACATAGCA
       CTCAACGAGA   ACGGGCCGCA   GTTATGCCCT   ATTATGGCGC   GGTGTATCGT

                                  XmnI
                             ~ ~ ~ ~ ~ ~ ~ ~
                             ~ ~ ~ ~ ~ ~ ~ ~

1151   GAACTTTAAA   AGTGCTCATC   ATTGGAAAAC   GTTCTTCGGG   GCGAAAACTC
       CTTGAAATTT   TCACGAGTAG   TAACCTTTTG   CAAGAAGCCC   CGCTTTTGAG

1201   TCAAGGATCT   TACCGCTGTT   GAGATCCAGT   TCGATGTAAC   CCACTCGCGC
       AGTTCCTAGA   ATGGCGACAA   CTCTAGGTCA   AGCTACATTG   GGTGAGCGCG

1251   ACCCAACTGA   TCCTCAGCAT   CTTTTACTTT   CACCAGCGTT   TCTGGGTGAG
       TGGGTTGACT   AGGAGTCGTA   GAAAATGAAA   GTGGTCGCAA   AGACCCACTC

1301   CAAAAACAGG   AAGGCAAAAT   GCCGCAAAAA   AGGGAATAAG   GGCGACACGG
       GTTTTTGTCC   TTCCGTTTTA   CGGCGTTTTT   TCCCTTATTC   CCGCTGTGCC

1351   AAATGTTGAA   TACTCATACT   CTTCCTTTTT   CAATATTATT   GAAGCATTTA
```

FIG. 35A-71

```
        TTTACAACTT ATGAGTATGA GAAGGAAAAA GTTATAATAA CTTCGTAAAT

                                                  BsrGI
                                                  ~~~~~

1401    TCAGGGTTAT TGTCTCATGA GCGGATACAT ATTTGAATGT ACATGAAATT
        AGTCCCAATA ACAGAGTACT CGCCTATGTA TAAACTTACA TGTACTTTAA

1451    GTAAACGTTA ATATTTTGTT AAAATTCGCG TTAAATTTTT GTTAAATCAG
        CATTTGCAAT TATAAAACAA TTTTAAGCGC AATTTAAAAA CAATTTAGTC

1501    CTCATTTTTT AACCAATAGG CCGAAATCGG CAAAATCCCT TATAAATCAA
        GAGTAAAAAA TTGGTTATCC GGCTTTAGCC GTTTTAGGGA ATATTTAGTT

1551    AAGAATAGAC CGAGATAGGG TTGAGTGTTG TTCCAGTTTG GAACAAGAGT
        TTCTTATCTG GCTCTATCCC AACTCACAAC AAGGTCAAAC CTTGTTCTCA

1601    CCACTATTAA AGAACGTGGA CTCCAACGTC AAAGGGCGAA AAACCGTCTA
        GGTGATAATT TCTTGCACCT GAGGTTGCAG TTTCCCGCTT TTTGGCAGAT

1651    TCAGGGCGAT GGCCCACTAC GAGAACCATC ACCCTAATCA AGTTTTTTGG
        AGTCCCGCTA CCGGGTGATG CTCTTGGTAG TGGGATTAGT TCAAAAAACC
                                                  BanII
                                                  ~~~~
```

FIG. 35A-72

```
1701   GGTCGAGGTG  CCGTAAAGCA  CTAAATCGGA  ACCCTAAAGG  GAGCCCCCGA
       CCAGCTCCAC  GGCATTTCGT  GATTTAGCCT  TGGGATTTCC  CTCGGGGGCT

1751   TTTAGAGCTT  GACGGGGAAA  GCCGGCGAAC  GTGGCGAGAA  AGGAAGGGAA
       AAATCTCGAA  CTGCCCCTTT  CGGCCGCTTG  CACCGCTCTT  TCCTTCCCTT

1801   GAAAGCGAAA  GGAGCGGGGCG  CTAGGGCGCT  GGCAAGTGTA  GCGGTCACGC
       CTTTCGCTTT  CCTCGCCCGC  GATCCCGCGA  CCGTTCACAT  CGCCAGTGCG

1851   TGCGCGTAAC  CACCACACCC  GCCGCGCTTA  ATGCGCCGCT  ACAGGGCGCG
       ACGCGCATTG  GTGGTGTGGG  CGGCGCGAAT  TACGCGGCGA  TGTCCCGCGC
                   NheI

1901   TGCTAGCGGA  GTGTATACTG  GCTTACTATG  TTGGCACTGA  TGAGGGTGTC
       ACGATCGCCT  CACATATGAC  CGAATGATAC  AACCGTGACT  ACTCCCACAG
                   XmnI                              AgeI

1951   AGTGAAGTGC  TTCATGTGGC  AGGAGAAAAA  AGGCTGCACC  GGTGCGGTCAG
       TCACTTCACG  AAGTACACCG  TCCTCTTTTT  TCCGACGTGG  CCACGCAGTC

2001   CAGAATATGT  GATACAGGAT  ATATTCCGCT  TCCTCGCTCA  CTGACTCGCT
       GTCTTATACA  CTATGTCCTA  TATAAGGCGA  AGGAGCGAGT  GACTGAGCGA
```

FIG. 35A-73

```
2051   ACGCTCGGTC GTTCGACTGC GGCGAGCGGA AATGGCTTAC GAACGGGGCG
       TGCGAGCCAG CAAGCTGACG CCGCTCGCCT TTACCGAATG CTTGCCCCGC

2101   GAGATTTCCT GGAAGATGCC AGGAAGATAC TTAACAGGGA AGTGAGAGGG
       CTCTAAAGGA CCTTCTACGG TCCTTCTATG AATTGTCCCT TCACTCTCCC

2151   CCGCGGCAAA GCCGTTTTTC CATAGGCTCC GCCCCCCTGA CAAGCATCAC
       GGCGCCGTTT CGGCAAAAAG GTATCCGAGG CGGGGGGACT GTTCGTAGTG

2201   GAAATCTGAC GCTCAAATCA GTGGTGGCGA AACCCGACAG GACTATAAAG
       CTTTAGACTG CGAGTTTAGT CACCACCGCT TTGGGCTGTC CTGATATTTC

2251   ATACCAGGCG TTTCCCCCTG GCGGCTCCCT CCTGCGCTCT CCTGTTCCTG
       TATGGTCCGC AAAGGGGGAC CGCCGAGGGA GGACGCGAGA GGACAAGGAC

                        AgeI
                        ~~~~~~

2301   CCTTTTCGTT TACCGGTGTC ATTCCGCTGT TATGGCCGCG TTTGTCTCAT
       GGAAAGCCAA ATGGCCACAG TAAGGCGACA ATACCGGCGC AAACAGAGTA

2351   TCCACGCCTG ACACTCAGTT CCGGGTAGGC AGTTCGCTCC AAGCTGGACT
       AGGTGCGGAC TGTGAGTCAA GGCCCATCCG TCAAGCGAGG TTCGACCTGA
```

FIG. 35A-74

```
2401  GTATGCACGA ACCCCCCGTT CAGTCCGACC GCTGCGCCTT ATCCGGTAAC
      CATACGTGCT TGGGGGGCAA GTCAGGCTGG CGACGCGGAA TAGGCCATTG

2451  TATCGTCTTG AGTCCAACCC GGAAAGACAT GCAAAAGCAC CACTGGCAGC
      ATAGCAGAAC TCAGGTTGGG CCTTTCTGTA CGTTTTCGTG GTGACCGTCG

2501  AGCCACTGGT AATTGATTTA GAGGAGTTAG TCTTGAAGTC ATGCGCCGGT
      TCGGTGACCA TTAACTAAAT CTCCTCAATC AGAACTTCAG TACGCGGCCA

2551  TAAGGCTAAA CTGAAAGGAC AAGTTTTAGT GACTGCGCTC CTCCAAGCCA
      ATTCCGATTT GACTTTCCTG TTCAAAATCA CTGACGCGAG GAGGTTCGGT

2601  GTTACCTCGG TTCAAAGAGT TGGTAGCTCA GAGAACCTAC GAAAAACCGC
      CAATGGAGCC AAGTTTCTCA ACCATCGAGT CTCTTGGATG CTTTTTGGCG

2651  CCTGCAAGGC GGTTTTTTCG TTTTCAGAGC AAGAGATTAC GCGCAGACCA
      GGACGTTCCG CCAAAAAAGC AAAGTCTCG TTCTCTAATG CGCGTCTGGT

                                     BglII

2701  AAACGATCTC AAGAAGATCA TCTTATTA
      TTTGCTAGAG TTCTTCTAGT AGAATAAT
```

FIG. 35A-75

M1: PCR using template

NoVspAatII: TAGACGTC

M2: synthesis

BIoxA-A: TATGAGATCTCATAACTTCGTATAATGTACGCTATACG-
AAGTTAT

BIoxA-B: TAATAACTTCGTATAGCATACATTATACGAAGTTATG-
AGATCTCA

M3: PCR, NoVspAatII as second oligo

XloxS-muta: CATTTTTTGCCCTCGTTATCTACGCATGCGATAACTTCGTA-
TAGCGTACATTATACGAAGTTATTCTAGACATGGTCATAGCTGTTTCCTG

M7-I: PCR

gIIINEW-fow: GGGGGGGAATTCGGTGGTGGTGGATCTGCGTGCGCTG-
AAACGGTTGAAAGTTG

gIIINEW-rev: CCCCCCCAAGCTTATCAAGACTCCTTATTACG

M7-II: PCR

gIIIss-fow: GGGGGGGGGAATTCGGAGGCGGTTCCGGTGGTGGC

M7-III: PCR

gIIIsupernew-fow: GGGGGGGGGAATTCGAGCAGAAGCTGATCTCT-
GAGGAGGATCTGTAGGGTGGTGGCTCTGGTTCCGGTGATTTTG

FIG. 35A-76

M8: synthesis

lox514-A: CCATAACTTCGTATAATGTACGCTATACGAAGTTATA

lox514-B: AGCTTATAACTTCGTATAGCGTACATTATACGAAGT-
TATGGCATG

M9II: synthesis

M9II-fow: AGCTTGACCTGTGAAGTGAAAAATGGCGCAGATT-
GTGCGACATTTTTTTTGTCTGCCGTTTAATTAAAGGGGGGGGT

M9II-rev: GTACACCCCCCCCCAGGCCGGCCCCCCCCCCCCCTTTAA-
TTAAACGGCAGACAAAAAAAAATGTCGCACAATCTGCG

M10II: assembly PCR with template

bla-fow: GGGGGGGGTGTACATTCAAATATGTATCCGCTCATG

bla-seq4: GGGTTACATCGAACTGGATCTC

bla1-muta: CCAGTTCGATGTAACCCACTCGCGCACCCAACTGATC-
CTCAGCATCTTTTACTTTCACC

blaII-muta: ACTCTAGCTTCCCGGCAACAGTTAATAGACTGGATG-
GAGGCGG

bla-NEW: CTGTTGCCGGGAAGCTAGAGTAAG

bla-rev: CCCCCCCTTAATTAAGGGGGGGGGGGCCGGCCATTATCAAA-
AAGGATCTCAAGAAGATCC

M11II/III: PCR, site-directed mutagenesis

FIG. 35A-77

f1-fow : GGGGGGGGGCTAGCACGCGCCCTGTAGCGGCGCATTAA

f1-rev: CCCCCCCTGTACATGAAATTGTAAACGTTAATATTTTG

f1-t133.muta: GGGCGATGGCCCACTACGAGAACCATCACCCTAATC

M12: assembly PCR using template

p15-fow: GGGGGGGAGATCTAATAAGATGATCTTCTTGAG

p15-NEWI: GAGTTGGTAGCTCAGAGAACCTACGAAAAACCGCCCTG-
CAAGGCG

p15-NEWII: GTAGGTTCTCTGAGCTACCAACTC

p15-NEWIII: GTTTCCCCCTGGCGGCTCCCTCCTGCGCTCTCCTGTTCCT-
GCC

p15-NEWIV: AGGAGGGAGCCGCCAGGGGGAAAC

p15-rev: GACATCAGCGCTAGCGGAGTGTATAC

M13: synthesis

BloxXB-A: GATCTCATAACTTCGTATAATGTATGCTATACGAAGTTA-
TTCA

BloxXB-B: GATCTGAATAACTTCGTATAGCATACATTATACGAAGTTA-
TGAGA

M14-Ext2: PCR, site-directed mutagenesis

ColEXT2-fow: GGGGGGGAGATCTGACCAAAATCCCTTAACGTGAG

Col-mutal: GGTATCTGCGCTCTGCTGTAGCCAGTTACCTTCGG

FIG. 35A-78

Col-rev: CCCCCCCGCTAGCCATGTGAGCAAAAGGCCAGCAA

M17: assembly PCR using template

CAT-1: GGGACGTCGGGTGAGGTTCCAAC

CAT-2: CCATACGGAACTCCGGGTGAGCATTCATC

CAT-3: CCGGAGTTCCGTATGG

CAT-4: ACGTTTAAATCAAAACTGG

CAT-5: CCAGTTTTGATTTAAACGTAGCCAATATGGACAACTTCTTC-GCCCCCGTTTTCACTATGGGCAAATATT

CAT-6: GGAAGATCTAGCACCAGGCGTTTAAG

M41: assembly PCR using template

LAC1: GAGGCCGGCCATCGAATGGCGCAAAAC

LAC2: CGCGTACCGTCCTCATGGGAGAAAATAATAC

LAC3: CCATGAGGACGGTACGCGACTGGGCGTGGAGCATCTGGTCGCA-TTGGGTCACCAGCAAATCCGCTGTTAGCTGGCCCATTAAG

LAC4: GTCAGCGGCGGGATATAACATGAGCTGTCCTCGGTATCGTCG

LAC5: GTTATATCCCGCCGCTGACCACCATCAAAC

LAC6: CATCAGTGAATCGGCCAACGCGCGGGGAGAGGCGGTTTGCGT4TTG-GGAGCCAGGGTGGTTTTTC

LAC7: GGTTAATTAACCTCACTGCCCGCTTTCCAGTCGGGAAACCTGTCGTGCC-AGCTGCATCAGTGAATCGGCCAAC

M41-MCS-fow: CTAGACTAGTGTTTAAACCGGACCGGGGGGGGGGCTT-AAGGGGGGGGGGGGG

FIG. 35A-79

M41-MCS-rev: CTAGCCCCCCCCCCCCCCTTAAGCCCCCCCCCGGTCCGGT-
TTAAACACTAGT

M41-fow: CTAGACTAGTGTTTAAACCGGACCGGGGGGGGGGCTTAA-
GGGCGGGGGGGG

M41-rev: CCCCCCCTTAAGTGGGCTGCAAAACAAAACGGCCTCC-
TGTCAGGAAGCCGCTTTTATCGGGTAGCCTCACTGCCCGCTTTCC

M41-A2: GTTGTTGTGCCACGCGGTTAGGAATGTAATTCAGCTCCGC

M41-B1: AACCGCGTGGCACAACAAC

M41-B2: CTTCGTTCTACCATCGACACGACCACGCTGGCACCCAGTTG

M41-C1: GTGTCGATGGTAGAACGAAG

M41-CII: CCACAGCAATAGCATCCTGGTCATCCAGCGGATAGTT-
AATAATCAGCCCACTGACACGTTGCGCGAG

M41-DI: GACCAGGATGCTATTGCTGTGG

M41-DII: CAGCGCGATTTGCTGGTGGCCCAATGCGACCAGATGC

M41-EI: CACCAGCAAATCGCGCTG

M41-EII: CCCGGACTCGGTAATGGCACGCATTGCGCCCAGCGCC

M41-FI: GCCATTACCGAGTCCGGG

M42: synthesis

Eco-H5-Hind-fow: AATTCCACCATCATCACCATTGACGTCTA

Eco-H5-Hind-rev: AGCTTAGACGTCAATGGTGATGATGGTGG

FIG. 35A-80